

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2005, 15:03:32 ; Search time 33.3983 Seconds
(without alignments)
3321.665 Million cell updates/sec

Title: RWHULB-A
Perfect score: 5953
Sequence: 1 MALRVLLLTALTLCGFNLD.....FKROYKDMSEGGPGAEPPQ 1153
Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5953	100.0	1153	1 RWHULB	cell surface glyco
2	4542	76.3	1153	2 S00551	leukocyte surface
3	3510	59.0	1163	1 RWHULC	cell surface glyco
4	1556	26.1	1170	2 S03308	cell surface glyco
5	1546	26.0	1163	2 I56126	lymphocyte fuction
6	1160	19.5	1179	2 A53213	integrin alpha-E c
7	1105.5	18.6	1151	2 A45226	integrin alpha-1 c
8	1096	18.4	1170	2 I45914	integrin alpha 2 s
9	1086	18.2	1178	2 S44142	VLA-2 protein homo
10	1084.5	18.2	1181	2 A33998	integrin alpha-2 c
11	1079	18.1	1180	2 A35854	integrin alpha-1 c
12	667	11.2	1039	2 A41131	lymphocyte-Peyer's
13	639	10.7	1038	2 S06046	integrin alpha-4 c
14	630	10.6	1035	2 I58409	integrin alpha-9 c
15	614.5	10.3	1041	2 T31437	integrin alpha cha
16	579.5	9.7	1054	2 J07294	alhap integrin -
17	573.5	9.6	1051	2 A35761	cell surface glyco
18	568.5	9.5	1053	2 I55534	VLA-3 alpha subuni
19	555.5	9.3	1053	2 S44250	integrin alpha-5 c
20	550	9.2	1034	2 A36108	integrin alpha-v c
21	533	9.0	1044	2 T10050	integrin alpha-v c
22	532	8.9	1049	2 A27079	fibronectin recept
23	532	8.9	1073	2 B36429	integrin alpha-6 c
24	529.5	8.9	1051	2 A40021	integrin alpha-3 c
25	528.5	8.9	1072	2 A38457	integrin alpha-6 c
26	525.5	8.8	1091	2 A41543	integrin alpha-6 c
27	524.5	8.8	1048	2 A27421	integrin alpha-5 c
28	517	8.7	1044	2 S16516	integrin alpha-8 c
29	506	8.5	1394	2 A29637	position-specific

30	496.5	8.3	1146	2 S40311	integrin - fruit f
31	495.5	8.3	1039	2 A34269	integrin alpha-2b
32	493.5	8.3	1037	2 A60163	glycoprotein IIB -
33	492	8.3	1137	2 JC5950	integrin alpha-7 c
34	488	8.2	1135	2 I61186	alpha-7 integrin -
35	486	8.2	126	2 B30892	leukocyte adhesion
36	474.5	8.0	1226	2 S44824	FS4r2.1 protein -
37	473	7.9	1106	2 S38783	integrin alpha cha
38	454.5	7.6	1139	2 S28277	hypothetical prote
39	452	7.6	1045	2 S60571	integrin alpha v c
40	433.5	7.3	1115	2 T09433	integrin alpha cha
41	426.5	7.2	1115	2 T09403	integrin alpha cha
42	391	6.6	764	2 I36916	glycoprotein IIB -
43	309	5.2	1086	2 T18523	integrin alpha cha
44	301.5	5.1	272	2 A55348	integrin alpha-1 -
45	299	5.0	604	2 I36917	glycoprotein IIB -

ALIGNMENTS

RESULT 1

RWHULB

cell surface glycoprotein CD11b precursor [validated] - human

N:Alternate names: complement receptor type 3 alpha chain; leukocyte adhesion protein Mac
eukocyte integrin alpha chain; neutrophil adherence receptor alphaM chain

C:Species: Homo sapiens (man)

C>Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text change 09-Jul-2004

C:Accession: A31108; A28915; A41600; A30892; A32218; A46526; A26091; I52567

R:Corbi, A.L.; Kishimoto, T.K.; Miller, L.J.; Springer, T.A.

J. Biol. Chem. 263, 12403-12411, 1988

A:Title: The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, CD11B).

A:Reference number: A31108; MUID:88315033; PMID:2457584

A:Accession: A31108

A:Molecule type: mRNA

A:Residues: 1-1153 <COR>

A:Cross-references: UNIPROT:P11215; GB:J03925; NID:g187284; PIDN:AAA59544.1; PID:g307148

A>Note: part of this sequence was confirmed by protein sequencing

R:Arnaout, M.A.; Gupta, S.K.; Pierce, M.W.; Tenen, D.G.

J. Cell Biol. 106, 2153-2158, 1988

A:Title: Amino acid sequence of the alpha subunit of human leukocyte adhesion receptor Mac-1.

A:Reference number: A28915; MUID:88257215; PMID:2454931

A:Accession: A28915

A:Molecule type: mRNA

A:Residues: 1-499,501-965,'P',967-1153 <ARN>

A:Cross-references: GB:M18044; GB:J03270; GB:M19664; GB:X07421; NID:g186935; PIDN:AAA594

A>Note: the authors translated the codon TAC for residue 1129 as Thr

A>Note: part of this sequence, including the amino end of the mature protein, was confir

R:Shelley, C.S.; Arnaout, M.A.

Proc. Natl. Acad. Sci. U.S.A. 88, 10525-10529, 1991

A:Title: The promoter of the CD11b gene directs myeloid-specific and developmentally regu

A:Reference number: A41600; MUID:92073318; PMID:1683702

A:Accession: A41600

A:Molecule type: DNA

A:Residues: 1-9 <SHE>

A:Cross-references: GB:M76724; NID:g180018; PIDN:AAA58410.1; PID:g553215

R:Arnaout, M.A.; Remold-O'Donnell, E.; Pierce, M.W.; Harris, P.; Tenen, D.G.

Proc. Natl. Acad. Sci. U.S.A. 85, 2776-2780, 1988

A:Title: Molecular cloning of the alpha-subunit of human and guinea pig leukocyte adhesi

A:Reference number: A94193; MUID:88190151; PMID:2833753

A:Accession: A30892

A:Molecule type: mRNA

A:Residues: 917-1042 <AR2>

A:Cross-references: GB:M18044

R:Hickstein, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J.

Proc. Natl. Acad. Sci. U.S.A. 86, 257-261, 1989

A:Title: cDNA sequence for the alphaM subunit of the human neutrophil adherence receptor

A:Reference number: A32218; MUID:89098993; PMID:2563162

A:Accession: A32218

A:Molecule type: mRNA

A:Residues: 9-1153 <HIC>

A:Cross-references: GB:J04145; NID:g189068; PIDN:AAA59903.1; PID:g386975

A>Note: part of this sequence was confirmed by protein sequencing
 R:Fleming, J.C.; Pahl, H.L.; Gonzalez, D.A.; Smith, T.F.; Tenen, D.G.
 J. Immunol. 150, 480-490, 1993
 A>Title: Structural analysis of the CD11b gene and phylogenetic analysis of the alpha-in
 n during evolution.
 A:Reference number: A46526; MUID:93123748; PMID:8419480
 A:Accession: A46526
 A>Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-499,501-1153 <FLE>
 A:Cross-references: GB:S52227; NID:g263047; PIDN:AAS24821.1; PID:g263049
 A>Note: the last three bases of intron 13, CAG, are included in some but not all mature
 A>Note: sequence extracted from NCBI backbone (NCBI:121963)
 R:Pierce, M.W.; Remold-O'Donnell, E.; Todd III, R.F.; Arnaout, M.A.
 Biochim. Biophys. Acta 874, 368-371, 1986
 A>Title: N-terminal sequence of human leukocyte glycoprotein Mol: conservation across sp
 A:Reference number: A90664; MUID:87076671; PMID:3539202
 A:Accession: A26091
 A:Molecule type: protein
 A:Residues: 17-31 <PIE>
 A:Experimental source: granulocytes
 R:Pahl, H.L.; Rosmarin, A.G.; Tenen, D.G.
 Blood 79, 865-870, 1992
 A>Title: Characterization of the myeloid-specific CD11b promoter.
 A:Reference number: 152567; MUID:92144986; PMID:1346576
 A:Accession: 152567
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-9 <RES>
 A:Cross-references: GB:M84477; NID:g180184; PIDN:AAA51960.1; PID:g553219
 C:Comment: A common beta chain (CD18) forms a heterodimer with this chain to form Mac-1
 C:Genetics:
 A:Gene: GDB:ITGAM; CR3A
 A:Cross-references: GDB:120599; OMIM:120980
 A:Map position: 16p11.2-16p11.2
 A>Note: promoter contains a GATA motif and two Sp1 consensus binding sites
 C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat hom
 C:Keywords: alternative splicing; calcium; cell adhesion; glycoprotein; heterodimer; mag
 F:1-16/Domain: signal sequence #status predicted <SIG>
 F:17-1153/Product: cell surface glycoprotein CD11b #status experimental <MAT>
 F:17-1108/Domain: extracellular #status predicted <EXT>
 F:148-318/Domain: von Willebrand factor type A repeat homology <VWA2>
 F:465-473/Region: calcium/magnesium binding #status predicted
 F:530-538/Region: calcium/magnesium binding #status predicted
 F:593-601/Region: calcium/magnesium binding #status predicted
 F:1109-1134/Domain: transmembrane #status predicted <TM>
 F:1135-1153/Domain: intracellular #status predicted <INT>
 F:86,240,391,469,693,697,735,802,881,901,912,941,947,979,994,1022,1045,1051,1076/Binding

Query Match 100.0%; Score 5953; DB 1; Length 1153;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MALRVLLLTALTLCHGFNLDTENAMTFQENARGFQSVVQLQGRVVVVGAPQEIIVAAQR 60
 DB 1 MALRVLLLTALTLCHGFNLDTENAMTFQENARGFQSVVQLQGRVVVVGAPQEIIVAAQR 60
 QY 61 GSLVQCDYSTGSCPIRLQVPVEAVNMSLGLSLAATTSPPQLACGPTVHTCSENTVVK 120
 DB 61 GSLVQCDYSTGSCPIRLQVPVEAVNMSLGLSLAATTSPPQLACGPTVHTCSENTVVK 120
 QY 121 GLCFLFGSLNRQQQPKFPFALRGCPQEDSDIAFLIDGSGSIIPHDFFRMKEFVSTVMBQL 180
 DB 121 GLCFLFGSLNRQQQPKFPFALRGCPQEDSDIAFLIDGSGSIIPHDFFRMKEFVSTVMBQL 180
 QY 181 KSKTFLFSIMQYSEBFRIHFTFKFQNNPNRSLVKPTQLLGRTHATGIRKVVRELFN 240
 DB 181 KSKTFLFSIMQYSEBFRIHFTFKFQNNPNRSLVKPTQLLGRTHATGIRKVVRELFN 240
 QY 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQEL 300
 DB 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQEL 300

RESULT 2

S00551

leukocyte surface glycoprotein Mac-1 alpha chain precursor - mouse

N:Alternate names: complement-3 receptor alpha chain

C:Species: Mus musculus (house mouse)

C>Date: 30-Sep-1989 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004

C:Accession: S00551; I59078

R:Pytela, R.

EMBO J. 7, 1371-1378, 1988

A>Title: Amino acid sequence of the murine Mac-1 alpha chain reveals homology with the ir

A:Reference number: S00551; MUID:88312584; PMID:3044779

A:Accession: S00551

A:Molecule type: DNA
A:Residues: 1-1153 <UNT>
A:CROSS-references: UNIPROT:P05555; EMBL:X07640; NID:G52982; PIDN:CAA30479.1; PID:G52983
A:Note: the authors translated the codon CAC for residue 569 as Gln
R:Saetre, L.; Roman, J.M.; Teplov, D.B.; Dreyer, W.J.; Gee, C.E.; Larson, R.S.; Roberts,
Proc. Natl. Acad. Sci. U.S.A. 83, 5644-5648, 1986
A:Title: A partial genomic DNA clone for the alpha subunit of the mouse complement recep
A:Reference number: I59078; MUID:86287312; PMID:2942940
A:Accession: I59078
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 11-44 <RES>
A:CROSS-references: GB:M14293; NID:G198993; PIDN:AAA39484.1; PID:G554193
C:Genetics:
C:Gene: Mac-1
C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat hom
C:Keywords: cell adhesion; glycoprotein; transmembrane protein
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-1153/Product: leukocyte surface glycoprotein Mac-1 alpha chain #status experimental
F:148-318/Domain: von Willebrand factor type A repeat homology <VWA2>
F:1106-1129/Domain: transmembrane #status predicted <TM>

Query Match 76.3%; Score 4542; DB 2; Length 1153;
Best Local Similarity 74.4%; Pred. No. 28-303;
Matches 859; Conservative 142; Mismatches 151; Indels 2; Gaps 2;

QY 1 MALRVLLLTALTLCHGFNLDENAMTFQENARGFGQVVQLOGSRVVGAPQEI1VAANOR 60
DB 1 MTLKALLVTAALCHGFNLDTEHPMTFQENAKGFQNVVQLGTSVVVAAPQEAQAVNQT 60
QY 61 GSLYQCDYSTGCEPIRLQVPVEAVNMSLGLSLAATTSPQLLACGPTVHTQCSNTYVK 120
DB 61 GALYQCDYSTSRCHPIPLQVPPEAVNMSLGLSLAVSTVPQQLLACGPTVHTQCKENTYV 120
QY 121 GLCFPLGSLNRQOPKFPFALRGCPQEDSDIAFLIDGSGIIPHPFRMKFVSTWEO 180
DB 121 GLCYLFGSNLLRPPQFPALRECPQESDIIVFLIDGSGINIIDFQMKFVSTWEO 180
QY 181 KSKTFLSLMQSYSEBFRHFTPEKQNNPNRSLVKPIITQLLGRTHATGIRKVVRELFN 240
DB 181 KSKTFLSLMQSYSEBFRHFTPEKQNNPNRSLVKPIITQLLGRTHATGIRKVVRELFH 240
QY 241 ITNGARKAFKLVITDGEKGDPLGVDVPEADREGVIIRYVGVGDAFSEKSRQEL 300
DB 241 KTNARENAAKLVITDGEKGDPLGVDVPEADREGVIIRYVGVGDAFSEKSRREL 300
QY 301 NTIAKPPRDHVFQNNPEALATIQNLREKXFALEGTTGSSSFEHMSQEGFSAIT 360
DB 301 DTIAKPGAEHVQVDNFALNTIQNLQEKIFALEGTTGSSSFEHMSQEGFSASIT 360
QY 361 SNGPLLLSTVGSYDAGGVPLVYTSKEKSTPINNTRVDSMDNDAYLGVAAILLRNVQSIV 420
DB 361 SNGPLLGSGVDFWAGGAPLYTSKDKVTFINTRVDSMDNDAYLGVAAILLRNVQSIV 420
QY 421 LGAPRYQHIGLVAMPFRONTGMESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLIGAP 480
DB 421 LGAPRYQHIGLVAMPFRONTGMESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLIGAP 480
QY 481 HYTEOTRGQVSVCPILRGQARWOCDAVLGCEQGPWGRFGAALTIVLGVNDGDKLTQVA 540
DB 481 HYTEKTRGQVSVCPILRGQARWOCDAVLGCEQGPWGRFGAALTIVLGVNDGDKLTQVA 540
QY 541 IGAPGEENRGAVALFHTGTSGSGISPSHSQRIAGSKLSPLRQYFGQSLSGGQDLTWDGIV 600
DB 540 IGAPGEENRGAVALFHTGTSGSGISPSHSQRIAGSKLSPLRQYFGQSLSGGQDLTWDGIV 600
QY 601 DLTVGAQGHVLLRQSVPLRVKVAIMEFNPVARNVFECDQVVGKAGEVRVCLHVQK 660
DB 600 DLAVGAQGHVLLRQSVPLRVKVAIMEFNPVARNVFECDQVVGKAGEVRVCLHVQK 660
QY 661 SPDRRLREGIQSVVTVYDIALDGRPHSPAVNETKSNTRCTOVGLTQTCETLKLQLP 720
DB 660 NTKDRREGDIQSVVTVYDIALDGRPHSPAVNETKSNTRCTOVGLTQTCETLKLQLP 720

RESULT 3

RWHULC

cell surface glycoprotein CD11c precursor - human

N:Alternate names: leukocyte adhesion receptor p150.95 alpha chain

C:Species: Homo sapiens (man)

C:Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text_change 09-Jul-2004

C:Accession: A35584; A35543; S00864

R:Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A.

J. Biol. Chem. 265, 12750-12751, 1990

A:Reference number: A36584

A:Contents: erratum

A:Accession: A36584

A:Molecule type: DNA

A:Residues: 1-1163 <COR>

A:CROSS-references: UNIPROT:P20702

A:Note: this revision to the sequence from reference A35543 includes the carboxyl end

R:Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A.

J. Biol. Chem. 265, 2782-2788, 1990

A:Title: Genomic structure of an integrin alpha subunit, the leukocyte p150.95 molecule.

A:Reference number: A35543; MUID:90153906; PMID:2303426

A:Accession: A35543

A:Molecule type: DNA

A:Residues: 1-834 <CO2>

A:Note: this sequence has been revised in reference A36584

R:Corbi, A.L.; Miller, L.J.; O'Connor, K.; Larson, R.S.; Springer, T.A.

EMBO J. 6, 4023-4028, 1987

A:Title: cDNA cloning and complete primary structure of the alpha subunit of a leukocyte

A:Reference number: S00864; MUID:88166645; PMID:3327687

A:Accession: S00864

A:Molecule type: mRNA

A:Residues: 1-755, 'L', 757-1163 <CO3>

A:CROSS-references: GB:M81695; EMBL:Y00093; NID:9487829; PIDN:AAA59180.1; PID:9487830

A:Note: part of this sequence was confirmed by protein sequencing

C:Comment: A common beta chain (CD18) forms a heterodimer with CD11b to form Mac-1 on mye

C:Genetics:

A:Gene: GDB:ITGAX; CD11C

A:CROSS-references: GDB:119758; OMIM:151510

A:Map position: 16p11.2-16p11.2

C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homo

C;Keywords: calcium; cell adhesion; glycoprotein; heterodimer; tandem repeat; F;1-19/Domain: signal sequence #status predicted <SIG> F;20-1163/Product: cell surface glycoprotein C11c #status predicted <MAT> F;20-1107/Domain: extracellular #status predicted <EXT> F;149-319/Domain: von Willebrand factor type A repeat homology <VWA4> F;1108-1133/Domain: transmembrane #status predicted <TM> F;1134-1163/Domain: intracellular #status predicted <INT> F;61,89,392,697,735,899,939,1050/binding site: carbohydrate (Asn) (covalent) #status predicted

[illegible]

QY 905 ENMPRTKTEFQLPVPKYAVIMVVTSHGVSTKYLNFTAS-ENTSRVMOHQYOVSNLQG 963
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 903 ENNTPTSKTTFQLPLPKVIAYTVYTSSHEQTTKYLNFSESEBEKSHVAMHRYQVNVLGQ 962
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 964 RSLPSLVFLPVRLNQTWIDRPQVTFEGENLSSTCHTXERLPSSHDSDFLAELRKAPVVNC 1023
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 963 RDLPSVINFWPELVNQEAIVMDVEVSHDPQNFSLRCSSEKIADPPADFLLAHIOKNPVLDIC 1022
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1024 SIACVQRIOCDIPFGIGIEEFNATLKGNLSFDWYIKTNSHNLIIVSTAETLFNDVSFTLL 1083
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1023 STAGCLRFRCDPSPSVQBELDFTLKGNLSFGWRVQILKKVSWVSVAEITFTDTSVYSOL 1082
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1084 PQGGAFVRSOQETKVPEVPNPPLIIVGVSSVGGLILLALITAALKLGFFFKROYKDMMMS 1143
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1083 PQGEAFMRQAQTTVLEUKYKHVNPTPLIVGSSIGGLLLALLITAVLYKGVFVKROKEMME 1142
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1144 E 1144
 ↓
Db 1143 E 1143

RESULT 4

S03308
cell surface glycoprotein CDlla precursor - human
N:Alternate names: leukocyte adhesion glycoprotein LFA-1 alpha chain; leukocyte function C:Species: Homo sapiens (man)
C>Date: 28-Feb-1990 #sequence revision 28-Feb-1990 #text_change 09-Jul-2004
C:Accession: S03308; A47458; A47565; A48759; S36044
R:Larson, R.S.; Corbi, A.L.; Berman, L.; Springer, T.
J. Cell Biol. 108, 703-712, 1989
A>Title: Primary structure of the leukocyte function-associated molecule-1 alpha subunit:
A:Reference number: S03308; MUID:89139587; PMID:2537322
A:Accession: S03308
A:Molecule type: mRNA
A:Residues: 1-1170 <LAR>
A:Cross-references: UNIPROT:P20701; UNIPROT:Q9UBC8; EMBL:Y00796; NID:g31421; PIDN:CAA6874
A>Note: part of this sequence was confirmed by protein sequencing
R:Cornewell, R.D.; Gollahon, K.A.; Hickstein, D.D.
Proc. Natl. Acad. Sci. U.S.A. 90, 4221-4225, 1993
A>Title: Description of the leukocyte function-associated antigen 1 (LFA-1 or CD1la) prom
A:Reference number: A47458; MUID:93248261; PMID:8097887
A:Accession: A47458
A:Molecule type: DNA
A:Residues: 1-20 <COR>
A>Note: sequence extracted from NCBI backbone (NCBIN:130862, NCBIP:130863)
R/Shelley, C.S.; Parokhad, O.C.; Arnaout, M.A.
Proc. Natl. Acad. Sci. U.S.A. 90, 5364-5368, 1993
A>Title: Identification of cell-specific and developmentally regulated nuclear factors t
A:Reference number: A47565; MUID:93281759; PMID:8099450
A:Accession: A47565
A:Molecule type: DNA
A:Residues: 1-20 <SHE>
A:Cross-references: GB:M95609
R/Nueda, A.; Lopez-Cabrera, M.; Vara, A.; Corbi, A.L.
J. Biol. Chem. 268, 19305-19311, 1993
A>Title: Characterization of the Cdlla (alphaL, LFA-lalpa) integrin gene promoter.
A:Reference number: A48759; MUID:93374910; PMID:8103515
A:Accession: A48759
A:Molecule type: DNA
A:Residues: 1-20 <NU&>
A:Cross-references: EMBL:Z22804; NID:g311405; PIDN:CAA80461.1; PID:g311406
C:Genetics:
A:Gene: GDB:ITGAL; CD1la
A:Cross-references: GDB:l19757; OMIM:153370
A:Map position: l6p11.2
C:Superfamily: cell surface glycoprotein CD1lb; von Willebrand factor type A repeat homol
C:Keywords: cell adhesion; cytoskeleton; glycoprotein; heterodimer; surface antigen; trar
F:1-25/Domin: signal sequence #status predicted <SIG>
F:26-1170/Product: leukocyte adhesion glycoprotein LFA-1 alpha chain #status predicted <NA
F:154-317/Domai: von Willebrand factor type A repeat homology <VWA2>

Query Match 26.1%; Score 1556; DB 2; Length 1170;
Best Local Similarity 34.3%; Pred. No. 3.1e-98;

Matches 409; Conservative 211; Mismatches 464; Indels 110; Gaps 38;	
QY	6 LLLTALTLCHEG-----NLDTENAMTFQ--ENARGFGQSVVQLQGRVVVVGAPQEI 54
Db	6 ITVMAMALLSGFFFPAPASSYNLDVRGARSFPPRAGRHFGYRVLQV-GNGVIVGAPGE- 63
QY	55 VAANQSGSYQCDYSTGSCPEIRLQVPVEAVNMSLGLSLAANTSPOLLACGPTVHQTC 114
Db	64 --GNSTGSLYQCSGTGHLCPVTLR-GSNYTSKYLGMTLATDPTDGSILACDGLSRTCD 120
QY	115 ENTYYKGLCLFLGSLNR-----QOPQKFPFALRGCPQEDSDIAFLJDGSGSIIPHPFRMK 170
Db	121 QNTYLSGLCYLFRQNLQGMQLQRPQFCIKG-----NVDLFLFDGMSLQDFBQKIL 176
QY	171 EFVSTVMEQLKSKTLFSLMQSYSEBPRIHFTFKFQNNPNRSLVKPIPTQLLGRTHRTATG 230
Db	177 DPMKDVMMKLSNTSYQFAAVQFSTSYKTEFSDSYVKKWDPDALLKHVKHMLLINTFGA 236
QY	231 IRKVVRELFNITNGARKNAFKILVITDGEKFGDPLGYEDVITPEADREGVIYRVIGVGA 290
Db	237 INYVATEVFREELGARPDATKVLIIITDGE--ATDSGNIDAAD-----IIRYIIGIKH 289
QY	291 PRSEKSRQELNTIAISKPPEDHVPQVNNPEALKTIONQREKXFALEGTOGTGSSSFHEM 350
Db	290 FTKESQETLHFPASKPASEFVKILDTFEKLDLFTTELQKKIYVIEGTSKQDLTSFNMEL 349
QY	351 SOEGFSAITSGPLLSTVSGSDWAGGVP-LYTSKEKSTFINMTRVDSMDNAYLGYAAA 409
Db	350 SSSGISADLSRGHAVVGAGKADWAGGFLDLKADLQDDTFIGNEPLTPEVRAGLYGTYT 409
QY	410 -IILNRVQSLVLGAPRYOHIGLVAMFR--QNTGMWESNANVKGTQIGAYFASLCSVDV 466
Db	410 WLPSRQKTSLLASGAPRYOHMGRVLLFQBPQGGHWSQVQTHGTQIGSYFGGELCGVDV 469
QY	467 DSNGSTDVLVLGAPHYEYTRGQSVVCLPRGORARWQCDV--LYCEQOGQPWRFGA 524
Db	470 DQDGETELLICAPLIFYGEGRGVFIY-----QRRQLGFEESVLELQGDGFPVLRFGFA 524
QY	525 LTVLDVNGDKLTVDAIGAPGEDNRGAVYLPFGHTSGSGISPSHSQIRAGSKLSRLQV 584
Db	525 ITALTDINGDLVDVAVGAPLEE--QGAVYIFNGRHG-GLSPQPPQRIEGTVLSGIQWF 581
QY	585 GQSLGGQDLTWGDLVLTLAGQHVLLRLSQPVLRKVAIMEFNPREAVNVEFQNDQV 644
Db	582 GRSIHGVKLEGGDLADVAVGAESQIVLSSRPVDMVTLMSPSPAEIPVHEVEGCSYSTS 641
QY	645 -KGKEAGEVRVCLHVQKSRDRRLREGQIOSVVTYDLALDSGRPHSRVFNETKNSTRQT 703
Db	642 NQKKEGVNITICFQI-KSLYPOF-QGRLVANUTYTLQLDGHRTRRRGLFPQGRHELNRNI 699
QY	704 QVLGLTOTCETLKLQLPNCIEDVPSPVILRNFSL---VGTPLS--AFGN-----LRPVL 753
Db	700 AVT-TSMSCDTDFSPFPVCVDLIISPINVSINFLSWEEBGTDRDQRAQGDIPILRPSL 758
QY	754 ABDAQRLFTALPPFKNCGNDNICQDDLSITFSFMSLCLVVGGRPFNVTVTVRNDEG 813
Db	759 HSETWEI-----PFEKNCGEDKCCANLRVSPSPARSRALRTAFASLSVELSLNLEED 813
QY	814 SVRTQVTFPFFPLDLSYRKVSTLQNRQSQRSLACES--ASSTEVSGALKSTSCSINHPI 871
Db	814 AYVQLDLHFPPGLSFRKVEML---KPHSQIIPVSCUELPEERLLISRAL---SCNVSGPI 867
QY	872 FPENSEVTFNITFDVDSKASLGKLLKANVTSENN---MPRTNKTEFQLEPLPVKIYAVY 927
Db	868 FRAGHSVALQMMFNTLVNSSNGDSVELHANVTENNEDSLLEDNSATTI---IPILYIPIN 924
QY	928 MVVTSHGVTSTKYNLTASENTSRVMOHQVQV---SNLQORSIP-LSLPLVPLVRNLQVTY 983
Db	925 ILIQQEDSTLVSTFPGPKIHQVKMYQVRIQPSIHDNIPTELEAVGVGPQPSSEGP 984
QY	984 WDRPOVTVSENLSSTCHTK--ERLPSHSD--FLAELRKAPVNVCSIAVCQRQCQDIPFG 1039
Db	985 THQWSVQMEPPV--PCHVEDLERLDDAAEPCLPGALFRCPFV-----1024

QY	1040 IOEEFNATLKGNSLSPDWIKTSHNHLIVSTAIEILFNDSVFTLLPCQGFVARSQETKVE 1099
Db	1025 FRQEILVQVIGTLELVGREIAS-SMFSLCSSLISFNSSKHFLHYGSNASL-AQVVMKVD 1082
QY	1100 PREVENPILPLIVGSSVGGLLLLALITAAALYKLGFPKQRYKQKMMSEB-GPPGABP 1152
Db	1083 VYVERQMILYLYLSGIGGLLLLLLIFIVLYKVGFYKRNLERKMEAGRVNGP 1136
RESULT 5	
156126	
Lymphocyte fuction-associated molecule-1-alpha - mouse	
C:Species: Mus musculus (house mouse)	
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004	
A:Accession: I56126	
R:Kaufmann, Y.; Tseng, E.; Springer, T.A.	
J. Immunol. 147, 369-374, 1991	
A:Title: Cloning of the murine lymphocyte function-associated molecule-1 alpha-subunit ar	
A:Reference number: I56126; MUID:91268576; PMID:2051027	
A:Accession: I56126	
A:Status: preliminary; translated from GB/EMBL/DBJ	
A:Molecule type: mRNA	
A:Residues: 1-1163 <RES>	
A:Cross-references: UNIPROT:P24063; GB:M60778; NID:g198785; PIDN:AAA39426.1; PID:g198786	
C:Genes: LPA-1	
C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homol	
F:151-315/Domain: von Willebrand factor type A repeat homology <VWAL>	
Query Match 26.0%; Score 1546; DB 2; Length 1163;	
Best Local Similarity 34.1%; Pred. No. 1.5e-97;	
Matches 408; Conservative 217; Mismatches 464; Indels 106; Gaps 38;	
QY	1 MALRV-----LLLTALTTL----CHGFNLDTENAMTFQENA-RGFGQSVVQLQGRVVVVGAPQ 52
Db	1 MSFRIAGPRLLLGLQLFQAKAWSYNLDRPTQSLAQAGRHFGYQVLQIEDG-VVVGAPG 59
QY	53 EIVAAQNRGSLYQCDSYTGSCPEIRLQVPEVAVNMSLGLSLAATTSPOLLACGPTVHOT 112
Db	60 E---CDNTGGLYHCITSSEFCQPVSLH-GSNHTSKYLGMTLATDAKGSLLACDPLSRT 115
QY	113 CSENTYVKGCLPFGSNLRQQPKFPEALRGCPQSDSDIAFLIDGSGSIIPHDFRMKBF 172
Db	116 CDQNTYLSGLCYLFPQSLGEPMLQNRPAYQECMKGKVDLVFLFDGQSGLDRKDFEILEF 175
QY	173 VSTVMEQLKSKTLFSLMQSYSEBPRIHFTFKEP-QNNPNRSLVKPITOLLGRTHRTATGI 231
Db	176 MKDVNRKLSNTSYQFAAVQFSTDCTEFTFLDYVKQNRKPNPDVLLGVSQPMFLLTNTFRAI 235
QY	232 RKVRELFNITNGARKNAFKILVITDGEKFGDPLGYEDVIVEADREG-----VIRVV 284
Db	236 NYVVAHVFEESGARPDATKVLIIITDG-----EASDKGNISAAHDIRYI 281
QY	285 IGVGDADFSEKSRQBELNTIASKPPRDHVPQVNNFPAALKTIONQREKXFAIEGTQTGSS 344
Db	282 IGIGKHFVSVQKXTHIFASEPVEEFVKILDTFEKLDLFDLQRRIVAIIEGTRQDLT 341
QY	345 SPEHEMSQEGFSAATISNGPPLLSTVSGSDWAGGVP-LYTSKEKSTFINMTRVDSMDNDAY 403
Db	342 SFNMELSSSGISADLSKGHAVVGAVGAKDWAGGFLDLREDLQGGATVPGEPLTSVVRGGY 401
QY	404 LQYAAA-IILNRVQSLVLGAPRYOHIGLVAMFR--QNTGMWESNANVXGTQIGAYFGAS 460
Db	402 LGYTVAMWTSRSLPPLAAGAPRYOHVGOVLFFQAPBAGRRWNQTKIEGTQIGSVFGGE 461
QY	461 LCSVDVDNNGSTDVLVLGAPHYEYTRGQSVVCLPRGORARWQCDVAVLYGEQGPQWGR 520
Db	462 LCSVDLDQDGEAEILLIAPLFFGQRGRVFTY---QRRQSLFEMVSELQGDPPGPLGR 518
QY	521 FGAALTVLGDVNGDKLTVAVTAPCEEDNRGAVYLPFGHTSGSGISPSHSQIRAGSKLSPR 580
Db	519 FGAALTALTDINGDRLTVDVAVGAPLEE--QGAVYIFNGKPG-GLSPQPSQRIQGAQVFP 575

Qy	631	EVARNVFECDVQVVKKEAG--EYRVCLHVQ-KSTRDLRREGQIQSVVYDIALDSGRPH	68
Db	652	KVNIQKNCH---MEGKETVCINATVCFVKLKSKEDTIYEADLQ---YRVTLDSLRQI	704
Qy	688	SRVAFNET-----KNSTRQTVGLGLTQTCE TLKLQLPNCIEDVPSPVLRLNFSLVGT	741
Db	705	SRPFSGTQERKQVORNIIVRKSEC-----TKHSFYMLDKHDFQDSVR---ITLDFNLT-D	755
Qy	742	PLSAFGNLRPVLAEDAQRFLTALPFPEKKNCGNDNICQDDLSITFFMSLDCLVWGGPRE-	800
Db	756	PENG-----PVLDDSLPNSVHEYIIPFAKDCGKKEKICISDLSLHVATTEKDLLIVRSQDK	810
Qy	801	FNVTVTVRNDEGDSYRTQVTFPPFLDLSYRKVSTLQQRSSQRSLACESASSTEVSGAL	860
Db	811	FNVSLTVKNTKDSAYNTRTIWHYSPNLVFSGIEAIQKD-----SCSEN-----	853
Qy	861	KYSTSCSINHPIFPENSEVTFNITFDVDSKASLGN-KLLLLKANVTSENMMPRTNKTEFQLE	919
Db	854	HNITCKVGYPLRGEWTFKLLQFNQTSYLMENVTIYLSATSDSEEPETLSDNVVNIS	913
Qy	920	LPVKAYVMVVTSHGVSTKYLNFTASENSTRSMOQHYOVSN-----LQGRS-----	966
Db	914	IPVKEYEVLQFYS-SASEYHISIAANETVPVINSTEDIGNEINIFYLIRKSGSPMPPEL	972
Qy	967	PISLAVF-----LVPVRLNQTIVWDRQVTFSENLSSCTHKE-----RLPS	1000
Db	973	KLSTSFNMTSGNPVLYPTGLSS-----SENANCRPHIFEDPFSINSKGKMTT	1022
Qy	1008	HSDPLAELRAPVVCSTAVCQRICQDIPFFGIQD-----EFNATLK	104
Db	1022	STD---HLKRGITLDCNCKPATITCNLTSSDISQVNVSLILWKPTFKSYFSSNLNLTIR	107
Qy	1050	GNLSFDWYIKTSHNHLIIVSTAELFNDSVFTLLPGQAFVRSQRETQKVEPEVNPPLPL	110
Db	1079	GEL-----RSENASVLSSN-----OKRELAIQISDKGLPGRVL	111
Qy	1110	--IVGSGVGGILLALITAAALYKLGFKFRQYKDMWSE	1144
Db	1115	WVILLSAFAGLLLLMLLILALWKIGFFRKLKKRMEK	1151
<p>RESULT 8</p> <p>I45914</p> <p>integrin alpha 2 subunit - bovine (fragment)</p> <p>C/Species: Bos primigenius taurus (cattle)</p> <p>C/Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004</p> <p>C/Accession: I45914</p> <p>R/Kamata, T.; Puzon, W.; Takada, Y.</p> <p>J. Biol. Chem. 269, 9659-9663, 1994</p> <p>A/Title: Identification of putative ligand binding sites within the I-domain o</p> <p>A/Reference number: A54402; MUID:94193647; PMID:7511592</p> <p>A/Accession: I45914</p> <p>A/Status: preliminary; translated from GB/EMBL/DBDJ</p> <p>A/Molecule type: mRNA</p> <p>A/Residues: 1-1170 <AM></p> <p>A/Cross-references: UNIPROT:P53710; GB:I25886; NID:9439695; PIDN:AAB59255.1; P</p> <p>F;161-336/Domain: von Willebrand factor type A repeat homology <WVA2></p>			
<p>Query Match 18.4%; Score 1096; DB 2; Length 1170;</p> <p>Best Local Similarity 27.8%; Pred. No. 1.3e-66;</p> <p>Matches 339; Conservative 216; Mismatches 498; Indels 168; Gaps 47</p>			
Qy	11	LTLCHGFNLTENAWTQ-ENARFGQSVQL---QGSRVVVGAPQEIIVAAQNRGLSYOC	66
Db	13	LNCVAVNVGLPKAKIFSGPSSBQFGYAVQGFIPKGNWLLPWSGSPFKRMGMGVYKC	72
Qy	67	--DYSTGSCBIRLQ-----VPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSNT	117
Db	73	PVDLSITTCCKLNLTQSTSMNVNTEKTNMSLGLTLTRNVGTGGFLTCPPLWACQCSQY	132
Qy	118	YVKGCLCFGSNLRQQPKFPEALRGCPQEDSDIAFLIDGSGSIIPHDPFRMKFEVSTVM	177

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Db 133 YTTGVCSDVSPDF-QRTSFAPAVQCP-SFIDVVVVCDSESNISYPWD--AVKNFLEKVF 188
QY 178 EQLK--KSKTLFSLMOYSEEPRIHFTFKFQNNPNSRLVKPITOLL-----GRTHATGCI 231
Db 189 QGLDGTPTQWGLQYANNPRVFNLTFSKSD--EMIKATSTQFYGGDLTNTFFKAI 245
QY 232 RKVRELFNITNGARKNAFKIILVITDGBKFGDPLGYEDVPEADREGVIRVIGV----287
Db 246 QYARDTAYSTAAGRGPGATKVMVWVTDGESH-DGSKLKAVIDQCNDNITLRFIAVLGYL 304
QY 288 -GDAPRSEKSRQELNTIASKPRDRHVQVNNFEALQTONQURKXPAIEGTQTGSSSF 346
Db 305 NNNALDITKNLKEIKAIASIPTRHFNFVDSADLLEKAGTIGEQIFSIETGVQG-GDNF 363
QY 347 EHEMSQEGFSAIT--SNGPILLSVGSVDWAGGVFLYTSKESKSTFINMT--RVDSDMN-D 401
Db 364 QNEMSQVGSFSAEYSQNNILMLGAYDWSVTVQKTPHGHILIFSQAQFQILQDRHS 423
QY 402 AYLGVAAAIILNRVQSLVGLGAPRYOHIGLVAMFRONTGMESNANV-----KGTQIGA 455
Db 424 SYLGSVASISTGNSVHFVAGAPRANYTGOIVLYSVN-----ENGNTVVIQSORGDQIGS 478
QY 456 YFGASICSVDVDSNGSTDLVLIGAPHYYEOTR--GGQVSVCLPRQGRARWOCDAVLIGE 513
Db 479 YFGSVLCADVNNKDTITDVLVGLGAPMYNDLKKKEGRVLYFTITKG-ILNMH--QFLEGP 535
QY 514 QCPQWRFRGAALTVLGDVNGDKLTDVAIGAPGEDNRGAVLPHGTSGSGISPSHSORIA 573
Db 536 NGLNARFGSAIAALSDINWDGFNDVIVGSPLENQNSGAVIYNHGEHM-ILRYSQKIL 594
QY 574 GS--KLSPRLQVFGSLSGQDLTDGDLVLTGAGHVLNLLRSQFVLVRKAIMEFNPRE 631
Db 595 GSDRAFSSHLQVFRSLDQGLNGDSITDVSAGAFQVQVQLWSQSIAVSDVSFTPKK 654
QY 632 VARNVFECDQVVKKEAGEVCLHVQKSPDRLEGOIQSVVTDLALD-----SGRPH 687
Db 655 I--TLNKNAEI-----KLKCF--SAKFRPTNQNQVAVIYNTITIDEDQSSRVI 701
QY 688 SRAVENETKNSRRTQVLGLTQTCF--TLKLQPLNCIEDPVSPIVLRNFSL--VGRPL 743
Db 702 SGRGLFKNERNCLQKTMIVSQARQCEYIIHQEPS--DIISPLNLCWNISLENPGT--756
QY 744 SAFGNLRLPVLABDAORLFTALFPFKNGCNDNICODDLSTTF-----SPMSLDCLVVGGR 799
Db 757 -----NPALEAYSETVVFSPFHKCGDGDGVCISDLVNLVQQLPATQOQPFVSNQNK 810
QY 800 EPNVTVVRNDCEDSYRTQVTFPPDLISYRKVSTLQNRQSORSWRLACESASST-EVSG 858
Db 811 RLTFVQVLNKKESAYNTEIIVVDFSENLF-----ASWMPVDGTGTEVTCQIAS 858
QY 859 ALKSTSCSINHIPIPPENSEVTNITFDVDSKASLGNKLLKANVTSENMPRTNKTEPOL 918
Db 859 SQKSVTCNVGYPALKSKQVQVTFINFDNLQ-NLQNASISFRALSESQENMADNSVNL 917
QY 919 ELPVKAYVMVTSVGTSKYLNTFASENTSRVMOHQVQVNLQOR-----SLPI 968
Db 918 KLSLLYDAEIIHT-RSTNINFEVSLDGNVSSV-HSFE--DIGPKFTSFKVITGVSVPV 973
QY 969 SLVFLVPVRLNQTLVDRPQVTFSEN--LSSTCHTKE-----RLPSHS 1009
Db 974 SWA-----SVIIHPQTKDKRNPMLYTVGHTDQAGDISCEAEINPLKIGQTSVSV 1024
QY 1010 DFLAF-LRKAPVNGSIAVCQRIQCDIPFFGQEEFNATLKNLSFDWYIKTSHNHLIV 1068
Db 1025 SFKSENFRHIKELNCRATSCSNIMCWLRLQVKGEYFLNVSTRIWNGTFAASTQTQVLT 1084
QY 1069 STAEI-LFNDVSFTL-----LPGOGAFVRSQTETKVEPFE-VNPNPLPIVGVSSVGLLL 1120
Db 1085 AAAEIDTNPQIYVEENTVITP-----LTIMPKHEKVEYPTGTVGVSVIAGILL 1134
QY 1121 LALITAALYKLGFFKRYOKDM 1141
Db 1135 LLALVALIWLKLGFFKRYOKDM 1155
```

RESULT 9

S44142

VLA-2 protein homolog - mouse

C:Species: Mus musculus (house mouse)

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C:Accession: S44142

R:Edelman, J.M.; Chan, B.M.; Uniyal, S.; Onodera, H.; Wang, D.Z.; Damjanovich, L.; Latzei
submitted to the EMBL Data Library, January 1994A:Description: The mouse VLA-2 homologue supports collagen and laminin adhesion but not
A:Reference number: S44142

A:Accession: S44142

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1178 <DE>

A:Cross-references: UNIPROT:Q62469; EMBL:Z29987; NID:G473098; PID:CA82877.1; PID:G47305
F:169-344/Domain: von Willebrand factor type A repeat homology <VMA2>

Query Match

Best Local Similarity 18.2%; Score 1086; DB 2; Length 1178;

Matches 347; Conservative 210; Mismatches 492; Indels 188; Gaps 44;

Db QY 5 VLLTALTLCGPNLDTENAMTFQ-ENARGFGQSVQL---QGSRVVVGAPQEIIVANQR 60

Db 15 LMLVQGLINCLAYNVGLPGAKIFSGPSQEQFGYSVQQLTNPQGNWLLVGSWSPGFPENRM 74

QY 61 GSLYQC-DYSTGSCPEIRLQ-----VPVEAVNMSLGLSLAATTSPPLLACGPTVHQ 111

Db 75 GDVYKCPVDLFTATCEKLNQNSASISNVTBIKTNMSLGLTLTRNPGTGGFLTCGLWAH 134

QY 112 TCSENTYVKGICFLFGSNLRQOQP---KFPALRGCPQEDSDIAFLIDGSGSIIPHDPFR 168

Db 135 QCGNQYATGIC---SDVSPDFQFLTSFSAVQACPSL-VDVVVVCDSESNIVP--WEA 187

QY 169 MKEFVSTVMEOLK--KSKTLFSLMOYSEEPRIHFTFKFQNNPNSRLVKPITQLLG-RT 225

Db 188 VKNELVFTGLDITGPKKTQVALLQYANEPRIIFNLNDFETKEDVMQVATSETRQHGDLT 247

QY 226 HTATGIRKVVRELNITNGARKNAFKIILVITDCEKFGDPLGYEDVPEADREGVIRVI 285

Db 248 NTFRAIFARDYAYVQTSGGRPATKVMVWVTDGESH-DGSKLTVIQCCNDDBILRPI 306

QY 286 GV-----GDAPRSEKSRQELNTIASKPRDRHVQVNNFEALQTONQURKXKFAIEGTQT 340

Db 307 AVLGYLNRNALTDKNLKEIKAIASITPTERYFFNVDAEALKEKAGTLGEQIFSIETVQ 366

QY 341 GSSSFPEHMSQEGFSA--ALTSNGPILLSVTSVGDWAGGVFLYTSKESKSTFINMT--RVD 396

Db 367 G-GDNFQWEMAQVGSADYAPQNDILMLGAVGAFDWSGTLVQETSHKFPVIPPKQAFDQVL 425

QY 397 SDMN-DAVLGYAAAIILNRNVQSLVGLGAPRYOHIGLVAMFRONTGMESNANV---KGT 451

Db 426 QDRNHSFLGYSVAAISTEDGVHVFAGAPRANYTGOIVLYSVNK---QGNVTVIQSHRGD 482

QY 452 QIGAYFGASCLSDVDVDSNGSTDLVLIGAPHYYEOTR--GGQVSVCLPRQGRARWOCDAV 509

Db 483 QIGSVFGSVLCSVDVDKDTITDVLVGPATYMDLKKKEGKVLFTITKGLNQHQ---F 539

QY 510 LYBQOQGPWRFGAALTVLGDVNGDKLTDVAIGAPGEDNRGAVLPHGTSGSGISPSHS 569

Db 540 LEGPEGTGNARFGSAIAALSDINMDGFNDVIVGSPVENENSAGVYIYNHGGT-IRTKYS 598

QY 570 QRIAGSKLSRPR--LQYFGQSLSGQDLTMDGLVDLTGAGHVLNLLRSQFVLVRKAIMEF 627

Db 599 QKILGSGNARFRHLQFFGRSLDGYDGLNGDSITDVSIGALGQVQLMSQSIAADVAIALP 658

QY 628 NPREAVNRFECNDQVVKKEAGEVRYCLHVQKSTRDLREGQIQSVVTVYDLALD----S 683

Db 659 TP-----DKITLLNKDAKITLCLCFRAEFEPAGQNNQV--AILENMTLDADGHS 705

QY 684 GRPHSRAVFNETKNSRRTQVGLTQTCF--LKQLPNCIEDPVSPIVLRNFSLVGT 741

Db 706 SRVTRGVFRENSEFLQKNMVVNEVQKCEHHISIQKPS-----DVVNELDLRVDISLNP 762
Qy 742 PLSAFGNLRPVLAEADAQRLFTALFFPEKCNNDNICQDDLSL-----TFSPMSLDC 792
Db 763 GTS-----PALEAYSETVKVFSIFPYKEGSDGICISDLILDVQQLPAIQTSF-----811
Qy 793 LVVGGPRENVTVTVRNDEGSYRTQVTFPPPLDLSYRKVSTLQNRQSRWRLACESAS 852
Db 812 IVSNQNKRLTFSVILKNRGEAYNTVLAESFSENLF-----ASFSPVDGTE 859
Qy 853 ST-EVSGALKTSCSINPIPPENSEVTFNITFDVDSKASLGNKLLKANVTSENMPRT 911
Db 860 VTCEVGSQKSVTCVUGVGPALKSEOOVTFTFNFDNLQ-NLQQAANFQAFSESO--ET 916
Qy 912 NKTE--FOLELPVKYAVVMVTVSHGVSTKYLNTASENTSRVMQHYQVSNLQGR-----964
Db 917 NKADNSVSLTIPLLYDAELHLT-RSTNINFVEISSDENAPSVIK---SVEDIGPKPIFSL 972
Qy 965 -----SLPISLVFLV-----PVRLNQTVID 985
Db 973 KVTAGSAPVMAVLTIHIPQYTKENPLLYLTGIQDQAGDISCTAEINPLKLPHTA---1029
Qy 986 RPQVTF-SENLSTCHTKERLPSPHDLAEALRKAPVVMCSIAVCQRIQCDIPFFGIGEEF 1044
Db 1030 -PSVSFKNEFR---HTKE-----LDCRTTSCSNIITCWLKDLHKABY 1069
Qy 1045 NATLGNLSFDWIYIKTSHNNHLLIVTAEILFENDSVFTLLPGQGAFFVRSQTKVFPFV 1104
Db 1069 FINVTVRNRTFAASTFTQVLTAAEIDTHNPQLFVIEENAVTIPLMIMKPTKAEVP 1128
Qy 1105 NPLPIVGVSSVGLLLALITAAALYKLGFFKRYQYKDM 1141
Db 1129 T--GVIIIGSIAGILLAMTAGLWKLGFPRKRYKMM 1163

RESULT 10
A:33998
Integrin alpha-2 chain precursor - human
N:Alternate names: CD49b; platelet glycoprotein GPIa; VLA-2/collagen receptor alpha-2 ch
C:Species: Homo sapiens (man)
C:Date: 30-Mar-1990 #sequence revision 18-Sep-1992 #text_change 09-Jul-2004
C:Accession: A33998; B56793; A53117
R:Takada, Y.; Hemler, M.E.
J. Cell Biol. 109, 397-407, 1989
A:Title: The primary structure of the VLA-2/collagen receptor alpha (2)-subunit (platelet
A:Reference number: A33998; MUID:89308879; PMID:2545729
A:Accession: A33998
A:Molecule type: mRNA
A:Residues: 1-1181 <TAK>
A:Cross-references: UNIPROT:P17301; GB:X17033; NID:G33906; PIDN:CAA34894.1; PID:G33907
A:Note: The authors translated the codon GAT for residue 802 as Gln, GTC for residue 803
R:Catimel, B.; Parmentier, S.; Leung, L.L.; McGregor, J.L.
Biochem. J. 279, 419-425, 1991
A:Title: Separation of important new platelet glycoproteins (GPIa, GPIC, GPIC*, GPIIa an
A:Reference number: A56793; MUID:92061944; PMID:1953640
A:Accession: B56793
A:Molecule type: protein
A:Residues: 30-43 <CAT>
A:Experimental source: platelet
R:Zutter, M.M.; Santoro, S.A.; Painter, A.S.; Tsung, Y.L.; Gafford, A.
J. Biol. Chem. 269, 463-469, 1994
A:Title: The human alpha-2 integrin gene promoter. Identification of positive and negati
A:Reference number: A53117; MUID:94103255; PMID:8276836
A:Accession: A53117
A:Molecule type: DNA
A:Residues: 1-16, 'V', 18-21 <ZUT>
A:Cross-references: GB:L24121; NID:9400342; PIDN:AAA16619.2; PID:G4583535
A:Note: authors translated the codon GTA for residue 17 as Leu
C:Genes: GDB:ITGA2; CD49B
A:Cross-references: GDB:128031; OMIM:192974
A:Map position: 5q11.1-5q11.2
C:Keywords: cell adhesion; glycoprotein; heterodimer; transmembrane protein

P:1-29/Domain: signal sequence #status predicted <SIG>
F:30-1133/Domain: extracellular #status predicted <EXT>
F:172-347/Domain: von Willebrand factor type A repeat homology <VMA2>
F:1134-1154/Domain: transmembrane #status predicted <TM>
F:1155-1181/Domain: intracellular #status predicted <CT>
F:1105,112,343,432,460,475,699,1057,1074,1081/Binding site: carbohydrate (Asn) (covalent)

Query Match 18.2%; Score 1084.5; DB 2; Length 1181;
Best Local Similarity 27.2%; Pred. No. 7.9e-66;
Matches 338; Conservative 215; Mismatches 498; Indels 193; Gaps 44;

Qy 3 LRVLLLTALT-----LCHGFNLDTENAMTFQ-ENARGFGQSVVOL---QGSRVVVVGAPE 53
Db 11 LPLLLVLALSOGILNCCLAYNVGLPEAKIFGSPSEQFGYAVQQINPKGNLLLVGSPWS 70
Qy 54 IVAANQRGSLYQC--DYSTGCEPIRLQ-----VPVEAVNMSLGLSLAATTPSPQLLA 104
Db 71 GPFENRMDGVKCPVDLSTACEKLNLTSTISIPNVTEMKTNMSLGLILTRNMGTTGFLT 130
Qy 105 CGPTVHQTCSENTYKGLCFPLPGSNLRQOPKFPBALRGCPQEDSDIAFLIDGSGSIIPH 164
Db 131 CGPLMAOQCNGQYTTGVCSDISPDF-QLSASFSPATQCPSSL-IDVVVVCDESNSIYFW 188
Qy 165 DFRMKFVSTVMEQLK--KSKTLFSLMOYSEERLHTEFEFQNNPNRSLVVKPIQTOLL 222
Db 189 D--AVKNLFKPVQGLDIPGKTQVGLIQYANNPRVFNLTNYTKKEEMIVATSQTSQVG 246
Qy 223 G-RHTATGIRKVRLEFNITNGARKNAFKILVITDGEKFDPLGVEDVPEADREGVI 281
Db 247 GDLTNTFCAGIYQARYAYASAGGRRSATKVMVVVTDGESH-DGSMKXAVIDQCNDNL 305
Qy 282 RYVIGV-----GDAPRSEKSRQELNTIASKPRDHVFOVNNPEALKTTQNRKXPAIE 336
Db 306 RFGIAYLVGNALDITKNLKEIKELIASIPTERYFFNVDEAALLKAGTIGEIQFSIE 365
Qy 337 GTQTGSSSSPEHEMSOEGFSAITSNGP--LLSTVGSYDAGGVFLYTSKEKSTFINMT- 393
Db 366 GTVQG-GDNFOEMSQVFSADYSQNDILMGAVAGFGWGTIVQKTSHGHLIIFPKQAF 424
Qy 394 -RVSDDMN-DAYLGYAAAIILNRNVQSLVLAGAPRYQHIGLVAMFRQNTGMMESNANV---448
Db 425 DQILDQRNHSYLVGYSAVAISTGESTHFVAGAPRANYTGQIVLYSVN-----ENGNITVI 479
Qy 449 ---KGTQIGAYFGASLCSVDVDSNGSTDLVIGAPHYYEQTR--GGQVSVCPPLRGQAR 503
Db 480 QAHRGDQIGSYFGSVLCSDVDVKDTITDVLVAGAPMYSDLKKEGRVYLFITIKGILCO 539
Qy 504 WQCDAVLYGEOGPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAIVLFGTSGSG 563
Db 540 HQ---FLEGPGEIENTRFGSAIALSDINMDGNDVIVGSPLENQNSGAVIYINGHQT- 595
Qy 564 ISPSHSQRIAGS--KLSPRLQYFGQSLSGGQDLTMDGLVDTLVGAQGHVLLRSQPLRV 621
Db 596 IRTKYSQKILSDGDAFRSHLYQFGSLDGYDGLNGSDITDVSIGAFGVVQLWSQSIADV 655
Qy 622 KAIMEFNPREAVNFECNDQVVKKEAGEVRVCLHVOKSTRDRREGOIQSVTYVDLAL 681
Db 656 ATEASFTPEKI--TLVNKNAQII-----LKLCP-----SAKFRPTKQNNQVAIVNITL 702
Qy 682 D-----SGRPHSRVAVNETKNSRTRQTVLGLTQTC--ETLKLQPLNCIEDPVPVLRNL 735
Db 703 DADGFSRVTSRGLPKENNERCLQKNMVVNOAQSCPEHIYIQEFS---DVVNSLDLRVD 759
Qy 736 FSLVGTPLSAFGNLPVLAEDAQRLLFTALFPPEKCNKNDNICQDDLSITF-----SPMSLD 791
Db 760 ISLENPGTIS-----PALEAYSETAKVFSIPHKCGEDGLCISDLVDLRQIPRAEQEP 813
Qy 792 CLVWGGPREFNVTVTVRNDEGSYRTQVTFPPPLDLSYRKVSTLQNRQSRWRLACESA 851
Db 814 FIVSNQNKRLTFSVTLKKNRESAYNTGIVVDPSENLFF-----ASFSLPVDGT 861
Qy 852 SST-EVSGALKTSCSINHPIFPENSEVTFTITFDVDSKASLGNKLLKANVTSENMPR 910

Db 862 EVTCQVAASQSVACDVGPALKRQEQVTFINFDNLQ-NLQNOASISFQALSBSQEN 920
Qy 911 TNKTEFQLELPVKYAVVMVTSHTGVTYKLNFTASENTSRVMQHOYQVSNLQOR----- 964
Db 921 KADNLVNLKIPLLYDAEI-----HLTRSTNINFEYISSDGNVPSIVHSFEDVGPKFIFSLK 976
Qy 965 ----SLPISLVELV-----PVRNLQTVWDR 986
Db 977 VTTGSPVSMATVLIHIPOYTKKNPLMYLTGVQTDKAGDISCNADINPLKIGQI-----S 1032
Qy 987 POVTF-SENLSSTCHTKERLPKSHDFLAELKAPVWNCISIAVCQRIQCDIPFGIOBEFN 1045
Db 1033 SSVSKSENF-----HTKE-----LNCRTASCNVTCWLKDVHMKGEYF 1072
Qy 1046 ATLKGNLSPDWIKTSHNHLIVSTAEI-LFENDSVFTLLPGGAFVRSQTKVPEPFPV 1104
Db 1073 VNVTRINWTFASFTQTVQVLTAAAEINTYNEIYVI-----EDNTVITPLMIM 1122
Qy 1105 NP-----LP-LIVGSSVGGLLLLALITAALYKLGFFKROYKDM 1141
Db 1123 KPDEKAEVPTGVIGSIITAGILLALLLVAAILKWLKGGFFKRYEKM 1166

RESULT 11
A35854
Integrin alpha-1 chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 23-Oct-1990 #sequence_revision 13-Sep-1991 #text_change 09-Jul-2004
R:Accession: A35854; S11243
J. Rignatius, M.J.; Large, T.H.; Houde, M.; Tawil, J.W.; Barton, A.; Esch, F.; Carbonetto, J. Cell Biol. 111, 709-720, 1990
A:Title: Molecular cloning of the rat integrin alpha-1 subunit: a receptor for laminin A
A:Reference number: A35854; MUID:90338125; PMID:2380249
A:Accession: A35854
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1180 <IGN>
A:Cross-references: UNIPROT:P18614; GB:X52140; NID:G56493; PIDN:CAA36384.1; PID:G56494
A:Keywords: cell adhesion; cytoskeleton; transmembrane protein
F:170-345/Domain: von Willebrand factor type A repeat homology <VWA2>

Query Match 18.1%; Score 1079; DB 2; Length 1180;
Best Local Similarity 27.6%; Pred. No. 1.9e-65;
Matches 350; Conservative 200; Mismatches 484; Indels 234; Gaps 47;

Qy 6 LLLTALTLCGNLNTENAMTFQENARG-EGOSVQL-----QGSRVVVGAPQEIIVANQRG 61
Db 18 LTVILGFCVSNVDVKNMSFSGPVEDMFGYVQOYNEEGKWLIGSLVPGQPKARTG 77
Qy 62 SLVQCDYSTGCEP-IRLQVPVEA-----VNMSLGLSLAAVTSPPQLLACQPTVHQ 111
Db 78 DVMKCPVGRERAMPCKLDPNTSIPNVTEIKENWTFGSTL-VTPNPGGFLACQPLAY 136
Qy 112 TCSENTYVKGCLFPGSNLRQOPKFPALRGCPQEDSDIAFLIDGSGSIIPHDPFRMKE 171
Db 137 RCGHLHYTTGICSDVSPTFQVNVSPAP--VQECSTQ-LDIVILVDGNSIYP--WESVIA 191
Qy 172 FVSTWMEQLK--KSKTSLSMQYSEEFRIHTFTEKFNQNPNSRLVKPIITQLLG-RHTHA 228
Db 192 FLNDLLKRMWDIGPKQTQGVQYGENVTHEFNLNKYSSTEEVLVAANKIGRGGQLQMTA 251
Qy 229 TGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLGVEDVPEADREGVIRVIGVG 288
Db 252 LGIDTARKEAFTEARGARRGVKVMVITVDGESH-DNYRLKQVIOCDENIQRFESAIL 310
Qy 289 DAFR-----SEKSRQELNTIASKPRDRHVQVNNFEALTKTONQLREKXFAIEGTQTGSS 343
Db 311 GHYNRGLNSTEFKEFBEIKSASEPTEKHFNFVNSDELAVTVIKALGERIFALEATADQSA 370
Qy 344 SSFEHEMQSGFSAITNSGPLLSLVGSDVAGGVFLYTSKEKSTFINWT--RVDSDMND 401
Db 371 ASFEMESQTGFSAHYSQDVMVLGAVGAYDMGTVMQKAMQMVIPHNTTFQTEPAQWNE 430

RESULT 12

A41131

Lymphocyte-Peyer's patch adhesion molecule alpha 4 precursor - mouse

N:Alternate names: integrin alpha-4

C:Species: Mus musculus (house mouse)

C:Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 09-Jul-2004

C:Accession: A41131; S16742

R:Neuhaus, H.; Hu, M.C.T.; Hemler, M.E.; Takada, Y.; Holzmann, B.; Weissman, I.L.

J. Cell Biol. 115, 1149-1158, 1991

A:Title: Cloning and expression of cDNAs for the alpha subunit of the murine lymphocyte-

A:Reference number: A41131; MUID:92064645; PMID:1840602

A:Accession: A41131

Qy 402 ---AYLGAAAIILNRVQSLVGLGAPRYOHIGLVAMFRONTGMWESNANVKGTOIGAYFG 458
Db 431 PLASVLYGVTSNATIPGDLVLIAGOPRINHGVQVVIYKMGEDGNINILQTLGEGQIGSYFG 490
Qy 459 ASLCSVDVDSNGSTDLVIGAPHY-----YEQTR-GGQVSVCPLPRGQRA 502
Db 491 SVLTIDIDKDSYTDLLLVGAPMTMGTEKEBQGVVYVAVNQTRFEYQMSLEPIRQTCCS 550
Qy 503 RWQCDVLYGQGGQPWG-RFGAALTVLGDVNGDKLTVAICAPGEEDNRGAIVLPHFGTSG 561
Db 551 SLKONSCTKENKNPCPGARFGTAIAAVKDLNDFGVDFNDVVICAPLEDDHAGAVIYH-G 609
Qy 562 SGISPHSQRIAGSKLSRLQYFGQSGSLGGODLTMDGLVDLTGGAQGHVLLRLRSQPLVR 621
Db 610 KTIIEAQAQIPSGDGGDKTLAFQSGIHGENDLNGDGLTDTVIGLGAALFWARDVAVV 669
Qy 622 KAIIEFPNPREVARNVFECNDQVVGKEAG--EVRVCLHVQ-KSTRDLRREGQIQSVVYTD 678
Db 670 KVTWNFEFNKVINIQKNCR---VEGKETVCINATMCFHVKLSKEDSYEADLQ-----YR 722
Qy 679 LALDSGRPHSRVFNET-----KNSTRQTVLGLTQTCETLKLQLPNCI----- 723
Db 723 VTLDSLKQISRSFFSGTQERKIQRNITVRESE-----CIRHSFYMJDX 765
Qy 724 EDPVSPVILRLNFSILVGTPLSAFGNLRFLAEDAQRLLFTALFFPEKNCNGNDNICODLSI 783
Db 766 HDFQDSVRVTLDFNLT-DPENG-----PVLDDALPNSVHEHI PPAKDCGNKERCISDLTL 819
Qy 784 TFSFMSLDCLVVGGPPE-FNVTVTRNDGDSYQTPTFPFPDLDSYRKVSTLQNRQSR 842
Db 820 NVSTTEKSLLVKSGHDKFNKSVLTQKNGDSAYNTRTVVQHSPLNLI FSGIBEIOKD---- 875
Qy 843 SWRLACSSASSTEVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLL-LKAN 901
Db 876 ----SCSN-----QNITCRVGPFLRAGTFTFKILFQPNVSHLSNALIHLSAT 922
Qy 902 VTSNNPRTNKTPEQLPELVKAYV---YMVVTSHGVS-----KYLNTASNTSR 950
Db 923 SDSEPLESLNDNEVNISIPVKYEVGLQFYSSASEHHISVAANETIPEFINST--EDIGN 980
Qy 951 VMQHQYQVSNLQGRSLP---ISLVF-----LVPVRLNQTVWD-----RP--- 987
Db 981 EINVFTYIRKGRHPMPPELQLSIFPNLTADGYPLVPIG-----WSSSDNVNCRPSL 1034
Qy 988 -----OVTFSS-----ENLSSTCHTKERLPKSHDPLAELKAPVWNCSTAV 1027
Db 1035 EDPFGINSKKWTSKSEVLKRGTIQDCSSTC-----GVATTCSLLP 1077
Qy 1028 CQRIQCDI-----PFFGIQEF---NATLKNLSFDWIYIKTSHNHLIVSTAEILFNS 1078
Db 1078 SDSLQVNVVLLLWKPTF-IRAHFSSNLTLRGELK-----SENSLTLSSN----- 1123
Qy 1079 VPTLLPGGAFVRSQTKETKPEFVNPPLP--IVGSSVGGILLILALITAYLKLGFPRK 1136
Db 1124 -----RKELAIQISKDGLPGRVPLVWILLSAFAGLMLLLMLLILAKWIGKIFPR 1172
Qy 1137 QYKDMWSE 1144
Db 1173 PLKKKMEK 1180

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2005, 15:04:07 ; Search time 241.379 Seconds
(without alignments)
2748.409 Million cell updates/sec

Title: RWHULB-A
Perfect score: 5953
Sequence: 1 MALRVLTLTALTLCHGFNLD.....FKRQYKDMMSGGPPGAEPPQ 1153

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 02: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	5937.5	99.7	1152	1	ITAM_HUMAN	P1215	homo sapien
2	4542	76.3	1153	1	ITAM_MOUSE	P05555	mus musculus
3	4456	74.9	1151	2	Q9J130	Q9J130	rattus norv
4	3826.5	64.3	920	2	Q28984	Q28984	sus scrofa
5	3510	59.0	1163	1	ITAX_HUMAN	P20702	homo sapien
6	3452	58.0	1162	1	ITAD_HUMAN	Q13349	homo sapien
7	3358.5	56.4	1188	2	Q6KAS4	Q6KAS4	mus musculus
8	3349.5	56.3	1169	1	ITAX_MOUSE	BAD21383	mus musculus
9	3279.5	55.1	1161	1	ITAD_RAT	Q9QXH4	mus musculus
10	3279.5	55.1	1161	1	ITAD_BOVIN	Q9QYH7	rattus norv
11	1583	26.6	1165	1	ITAL_MOUSE	P61625	bos taurus
12	1560	26.2	1170	1	ITAH_HUMAN	P20701	homo sapien
13	1557	26.2	1166	2	Q6TYB8	Q6TYB8	bos taurus
14	1557	26.2	1166	2	AAQ90015	AAQ90015	bos taurus
15	1546	26.0	1163	1	ITAM_MOUSE	P24063	mus musculus
16	1542	25.9	1161	2	Q9WTV4	Q9WTV4	mus musculus
17	1531.5	25.7	1160	2	Q9R200	Q9R200	mus musculus
18	1416	23.8	1196	2	Q9RTF1	Q9RTF1	cyprinus ca
19	1365.5	22.9	1187	2	Q9RTF0	Q9RTF0	cyprinus ca
20	1358	22.8	1086	2	Q9GHB1	Q9GHB1	homo sapien
21	1274	21.1	927	2	Q8HZV0	Q8HZV0	bos taurus
22	1168.5	19.6	1167	2	O88340	O88340	rattus norv
23	1162.5	19.5	1167	1	ITAE_MOUSE	Q60677	mus musculus
24	1160	19.5	1179	1	ITAE_HUMAN	P38570	homo sapien
25	1122.5	18.9	1167	2	O88341	O88341	rattus norv
26	1105.5	18.6	1151	1	ITAI_HUMAN	P56199	homo sapien
27	1099.5	18.5	1189	1	ITAH_HUMAN	Q9UKX5	homo sapien
28	1096	18.4	1170	1	ITAD_BOVIN	P53710	bos taurus
29	1089.5	18.3	1178	2	O6PIC7	O6PIC7	mus musculus
30	1089.5	18.3	1178	2	AHH65139	AHH65139	mus musculus
31	1086	18.2	1178	1	ITAZ_MOUSE	Q62469	mus musculus

32	1084.5	18.2	1181	1	ITAZ_HUMAN	P17301	homo sapien
33	1082.5	18.2	1167	1	ITAG_HUMAN	O75578	homo sapien
34	1079	18.1	1180	1	ITAI_RAT	P18614	rattus norv
35	1065.5	17.9	1171	2	O42094	O42094	gallus gall
36	1057.5	17.8	1188	1	ITAH_MOUSE	P61622	mus musculus
37	1057.5	17.8	1188	2	Q7QC3	Q7QC3	mus musculus
38	1046	17.6	1038	2	Q8BS01	Q8BS01	mus musculus
39	1017	17.1	895	2	Q9WUF8	Q9WUF8	mus sp. itg
40	1014.5	17.0	1160	2	Q8MKF4	Q8MKF4	felis silve
41	865	14.5	348	2	Q8TES5	Q8TES5	homo sapien
42	849	14.3	1332	2	Q9BPQ8	Q9BPQ8	halocynthia
43	810.5	13.6	304	2	Q6PG66	Q6PG66	mus musculus
44	810.5	13.6	304	2	AHH57200	AHH57200	mus muscu
45	775	13.0	205	2	Q63001	Q63001	rattus norv

ALIGNMENTS

RESULT 1
ITAM_HUMAN
ID ITAM_HUMAN STANDARD; PRT; 1152 AA.
AC P11215;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor MOI)
DE (Neutrophil adherence receptor).
GN Name:ITGAM; Synonyms:CR3A, CD11B;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88315033; PubMed=2457584;
RA Corbi A.L., Kishimoto T.K., Miller L.J., Springer T.A.;
RT "The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, CD11b) alpha subunit. Cloning, primary structure, and relation to the integrins, von Willebrand factor and factor B.";
RL J. Biol. Chem. 263:12403-12411(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88190151; PubMed=2833753;
RA Arnaut M.A., Remold-O'Donnell E., Pierce M.W., Harris P., Tenen D.G.;
RT "Molecular cloning of the alpha subunit of human and guinea pig leukocyte adhesion glycoprotein Mol: chromosomal localization and homology to the alpha subunits of integrins.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:2776-2780(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88257315; PubMed=2454931;
RA Arnaut M.A., Gupta S.K., Pierce M.W., Tenen D.G.;
RT "Amino acid sequence of the alpha subunit of human leukocyte adhesion receptor Mol (complement receptor type 3).";
RL J. Cell Biol. 106:2153-2158(1988).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=93123748; PubMed=8419480;
RA Fleming J.C., Pahl H.L., Gonzalez D.A., Smith T.F., Tenen D.G.;
RT "Structural analysis of the CD11b gene and phylogenetic analysis of the alpha-integrin gene family demonstrate remarkable conservation of genomic organization and suggest early diversification during evolution";
RL J. Immunol. 150:480-490(1993).
RN [5]
RP SEQUENCE OF 9-1153 FROM N.A.
RX MEDLINE=89098893; PubMed=2563162;
RA Hackett D.D., Hickey M.J., Ozols J., Baker D.M., Back A.L., Roth G.J.;
RT "cDNA sequence for the alpha M subunit of the human neutrophil adherence receptor indicates homology to integrin alpha subunits.";

Proc. Natl. Acad. Sci. U.S.A. 86:257-261 (1989).
[6]
SEQUENCE OF 1-9 FROM N.A.
MEDLINE=92073318; PubMed=1683702;
RA Shelley C.S., Arnaout M.A.;
RT "The promoter of the CD11b gene directs myeloid-specific and
RT developmentally regulated expression.";
Proc. Natl. Acad. Sci. U.S.A. 88:10525-10529 (1991).
[7]
SEQUENCE OF 1-9 FROM N.A.
TISSUE=Blood;
RA MEDLINE=92144986; PubMed=1346576;
RA Paul H.L., Rosmarin A.G., Tenen D.G.;
RT "Characterization of the myeloid-specific CD11b promoter.";
Blood 79:865-870 (1992).
[8]
SEQUENCE OF 17-31.
RA MEDLINE=87076671; PubMed=3339202;
RA Pierce M.W., Remold-O'Donnell E., Todd R.F. III, Arnaout M.A.;
RT "N-terminal sequence of human leukocyte glycoprotein Mol: conservation
RT across species and homology to platelet IIb/IIIa.";
Biochim. Biophys. Acta 874:368-371 (1986).
[9]
X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 148-331.
RA MEDLINE=95171458; PubMed=7867070;
RA Lee J.O., Rieu P., Arnaout M.A., Liddington R.;
RT "Crystal structure of the A domain from the alpha subunit of integrin
RT CR3 (CD11b/CD18).";
Cell 80:631-638 (1995).
[10]
X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 148-334.
RA MEDLINE=96363671; PubMed=8747460;
RA Lee J.O., Bankston L.A., Arnaout M.A., Liddington R.C.;
RT "Two conformations of the integrin A-domain (I-domain): a pathway for
RT activation";
Structure 3:1333-1340 (1995).
[11]
X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 148-337.
RA MEDLINE=98362595; PubMed=9687375;
RA Baldwin E.T., Sarver R.W., Bryant G.L. Jr., Curry K.A.,
RA Fairbanks M.B., Finzel B.C., Garlick R.L., Heinrichson R.L.,
RA Horton N.C., Kelley L.L., Mildner A.M., Moon J.B., Mott J.E.,
RA Mutschler V.T., Tomich C.S., Watenpaugh K.D., Wiley V.H.;
RT "Cation binding to the integrin CD11b I domain and activation model
RT assessment.";
Structure 6:923-935 (1998).
[12]
3D-STRUCTURE MODELING OF 17-616.
RA MEDLINE=98226734; PubMed=9560195;
RA Oxvig C., Springer T.A.;
RT "Experimental support for a beta-propeller domain in integrin alpha-
RT subunit and a calcium binding site on its lower surface.";
Proc. Natl. Acad. Sci. U.S.A. 95:4870-4875 (1998).
CC -!- FUNCTION: Integrin alpha-M/beta-2 is implicated in various
CC adhesive interactions of monocytes, macrophages and granulocytes
CC as well as in mediating the uptake of complement-coated particles.
CC It is identical with CR-3, the receptor for the iC3b fragment of
CC the third complement component. It probably recognizes the R-G-D
CC peptide in C3b. Integrin alpha-M/beta-2 is also a receptor for
CC fibrinogen, factor X and ICAM-1. It recognizes F1 and P2 peptides
CC of fibrinogen gamma chain.
CC -!- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-M
CC associates with beta-2.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Predominantly expressed in monocytes and
CC granulocytes.
CC -!- DOMAIN: The integrin I-domain (inset) is a VWFA domain. Integrins
CC with I-domains do not undergo protease cleavage.
CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
CC -!- SIMILARITY: Contains 7 FG-GAP repeats.
CC -!- SIMILARITY: Contains 1 VWFA domain.
CC -!- SIMILARITY: Contains 1 VWFA domain.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD11b entry;
WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd11b.htm".

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or send an email to license@isb-sib.ch).

EMBL; J03925; AA59544.1; -
EMBL; M18044; AA59491.1; -
EMBL; J04145; AA59903.1; -
EMBL; S52227; AAB24821.1; -
EMBL; S52152; AAB24821.1; JOINED.
EMBL; S52153; AAB24821.1; JOINED.
EMBL; S52154; AAB24821.1; JOINED.
EMBL; S52155; AAB24821.1; JOINED.
EMBL; S52157; AAB24821.1; JOINED.
EMBL; S52159; AAB24821.1; JOINED.
EMBL; S52161; AAB24821.1; JOINED.
EMBL; S52164; AAB24821.1; JOINED.
EMBL; S52165; AAB24821.1; JOINED.
EMBL; S52167; AAB24821.1; JOINED.
EMBL; S52169; AAB24821.1; JOINED.
EMBL; S52170; AAB24821.1; JOINED.
EMBL; S52173; AAB24821.1; JOINED.
EMBL; S52174; AAB24821.1; JOINED.
EMBL; S52180; AAB24821.1; JOINED.
EMBL; S52181; AAB24821.1; JOINED.
EMBL; S52184; AAB24821.1; JOINED.
EMBL; S52189; AAB24821.1; JOINED.
EMBL; S52191; AAB24821.1; JOINED.
EMBL; S52192; AAB24821.1; JOINED.
EMBL; S52203; AAB24821.1; JOINED.
EMBL; S52212; AAB24821.1; JOINED.
EMBL; S52213; AAB24821.1; JOINED.
EMBL; S52216; AAB24821.1; JOINED.
EMBL; S52219; AAB24821.1; JOINED.
EMBL; S52220; AAB24821.1; JOINED.
EMBL; S52221; AAB24821.1; JOINED.
EMBL; S52222; AAB24821.1; JOINED.
EMBL; S52226; AAB24821.1; JOINED.
EMBL; M76724; AA59410.1; -
EMBL; M84477; AA51960.1; -
PIR; A31108; RWHLB.
PDB; 1A8X; Model; @=17-1152.
PDB; 1BHQ; X-ray; 1/2=-.
PDB; 1IDN; X-ray; 1/2=-.
PDB; 1IDO; X-ray; @=140-331.
PDB; 1JLM; X-ray; @=143-334.
PDB; 1MUU; X-ray; A=137-331.
PDB; 1MF7; X-ray; A=144-337.
PDB; 1N9Z; X-ray; A=140-335.
PDB; 1NAS; X-ray; A=144-345.
Genew; HGNC:6149; ITGAM.
MIM; 120980; -
GO; GO:0008305; C:integrin complex; TAS.
GO; GO:0007155; P:cell adhesion; TAS.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; VWF_A.
Pfam; PF01839; FG-GAP; 3.
Pfam; PF00092; VWA; 1.
PRINTS; PR01185; INTEGRIN.
PRINTS; PR00453; VWFADOMAIN.
SMART; SM00191; Int_alpha; 5.
SMART; SM00327; VWA; 1.
PROSITE; PS00242; INTEGRIN_ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
3D-structure; Calcium; Cell adhesion; Direct protein sequencing;
Glycoprotein; Integrin; Magnesium; Receptor; Repeat; Signal;
Transmembrane.

[illegible]

RX MEDLINE=86287312; PubMed=2942940;
 RA Sastre L., Roman J.M., Teplov D.B., Dreyer W.J., Gee C.E.,
 RA Larson R.S., Roberts T.M., Springer T.A.;
 RT "A partial genomic DNA clone for the alpha subunit of the mouse
 RT complement receptor type 3 and cellular adhesion molecule Mac-1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:5644-5648(1986).
 [4]
 RN SEQUENCE OF 17-28.
 RP MEDLINE=85188276; PubMed=3887182;
 RX Springer T.A., Teplov D.B., Dreyer W.J.;
 RA "Sequence homology of the LFA-1 and Mac-1 leukocyte adhesion
 RT glycoproteins and unexpected relation to leukocyte interferon.";
 RL Nature 314:540-542(1985).
 CC -!- FUNCTION: Integrin alpha-M/beta-2 is implicated in various
 CC adhesive interactions of monocytes, macrophages and granulocytes
 CC as well as in mediating the uptake of complement-coated particles.
 CC It is identical with CR-3, the receptor for the iC3b fragment of
 CC the third complement component. It probably recognizes the R-G-D
 CC peptide in C3b. Integrin alpha-M/beta-2 is also a receptor for
 CC fibrinogen, factor X and ICAM1. It recognizes p1 and p2 peptides
 CC of fibrinogen gamma chain. Alpha-M/beta-2 play a critical role in
 CC mast cell development and in immune complex-mediated
 CC glomerulonephritis. Mice expressing a null mutation of the alpha-M
 CC subunit gene demonstrate increase in neutrophil accumulation, in
 CC response to a impaired degradation and phagocytosis, events that
 CC apparently accelerate apoptosis in neutrophils. These mice develop
 CC obesity.
 CC -!- SUBUNIT: Heterodimer of an alpha and a beta chain. Alpha-M
 CC associates with beta-2.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P05555-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P05555-2; Sequence=VSP_010473;
 CC Note=No experimental confirmation available;
 CC -!- TISSUE SPECIFICITY: Predominantly expressed in monocytes and
 CC granulocytes.
 CC -!- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins
 CC with I-domains do not undergo protease cleavage.
 CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
 CC -!- SIMILARITY: Contains 7 FG-GAP repeats.
 CC -!- SIMILARITY: Contains 1 VWFA domain.
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

 DR EMBL; X07640; CAA30479.1; -;
 DR EMBL; AK039444; BAC30350.1; -;
 DR EMBL; M14293; AAA39484.1; -;
 DR PIR; S00551; S00551.
 DR HSSP; P11215; 1BHQ.
 DR MGD; MGI:96607; Itgam.
 DR GO; GO:0009897; C:external side of plasma membrane; IDA.
 DR GO; GO:0007155; P:cell adhesion; IMP.
 DR GO; GO:0045123; P:cellular extravasation; IMP.
 DR GO; GO:0030593; P:neutrophil chemotaxis; IMP.
 DR InterPro; IPR000413; Integrin_alpha.
 DR InterPro; IPR002035; VWF A.
 DR Pfam; PF01839; FG-GAP; 3.
 DR Pfam; PF00357; Integrin_alpha; 1.
 DR Pfam; PF00092; VWA; 1.
 DR PRINTS; PR01185; INTEGRINA.
 DR PRINTS; PR00453; VWFADOMAIN.
 DR SMART; SM00191; Int_alpha; 5.
 DR SMART; SM00327; VWA; 1.
 DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.

DR PROSITE; PS00234; VWFA; 1.
 KW Alternative splicing; Calcium; Cell adhesion;
 KW Direct protein sequencing; Glycoprotein; Integrin; Receptor; Repeat;
 KW Signal; Transmembrane.
 FT SIGNAL 1 16
 FT CHAIN 17 1153
 FT DOMAIN 17 1105
 FT TRANSMEM 1106 1129
 FT DOMAIN 1130 1153
 FT REPEAT 31 84
 FT REPEAT 85 163
 FT DOMAIN 164 350
 FT REPEAT 337 400
 FT REPEAT 401 452
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 FT REPEAT 517 575
 FT REPEAT 580 632
 FT CA_BIND 465 473
 FT CA_BIND 529 537
 FT CA_BIND 592 600
 FT SITE 1132 1136
 FT DISULFID 66 73
 FT DISULFID 105 123
 FT DISULFID 654 711
 FT DISULFID 770 776
 FT DISULFID 999 1023
 FT DISULFID 1028 1033
 FT CARBOHYD 58 58
 FT CARBOHYD 86 86
 FT CARBOHYD 391 391
 FT CARBOHYD 696 696
 FT CARBOHYD 734 734
 FT CARBOHYD 772 772
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 FT VARSPLIC 453 569
 FT CONFLICT 37 37 N -> S (in Ref. 2).
 FT CONFLICT 683 683 V -> G (in Ref. 2).
 SQ SEQUENCE 1153 AA; 127480 MW; 178DB988AECB0343 CRC64;
 Query Match 76.3%; Score 4542; DB 1; Length 1153;
 Best Local Similarity 74.4%; Pred. No. 3.9e-290;
 Matches 859; Conservative 142; Mismatches 151; Indels 2; Gaps 2;
 QY 1 MALRVLLTALTLCGHFNLDTENAMTQBNARGQSVVQLGSRVVVGAPQEIIVANQR 60
 DB 1 MTLKALLVTALALCHGFNLDTEHPMTQENAKGFQNVVLGGTSVVVAAPQEKAVNQ 60
 QY 61 GSLYQCDYSTGSCPIRLQVPEAVNMSLGLSLAATTSPPOLLACGPTVHTCSENTYVK 120
 DB 61 GALLYQCDYSTGSCPIPLQVPEAVNMSLGLSLAVSTVPQOLLACGPTVHTCSENTY 120
 QY 121 GLCFLFGSNLRQQPKFPPEALRGCPQEDSDIAFLIDGSGSIIPHDPRMKFVSTVMEQL 180
 DB 121 GLCYLFGSNLLRPPQFPPEALRGCPQESDIVFLIDGSGSINNTDFQMKFVSTVMEQ 180
 QY 181 KSKSTLFLSMQYSEEFRIHFTFKFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFN 240
 DB 181 KSKSTLFLSMQYSEDFRIHFTFNDKRNPSRSHVSPIKQLNGRTKTAGIRKVVREL 240
 QY 241 ITNGARNAFKILVITDGEKFGDPLGVEDVPEADREGVIRYVIGVDAPRSEKSRQEL 300
 DB 241 KTGARENAKILVITDGEKFGDPLGVEDVPEADREGVIRYVIGVNAFNPKQSRREL 300


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Db 301 DTIASKPAGHFVQVDFNFEALNTIQNLQEKIFAIEGTQTGSSSFHEHMSQEGFSASIT 360
Qy 361 SNGPLLSVGSVDWAGGVFLYTSKEKSTFINMTRVDSMDNDAYLGYAAAILLRNRVQSLV 420
Db 361 SNGPLLSVGSVDWAGGVFLYTSKDKVTFINTRVDSMDNDAYLGYAAAILLRNRVQSLV 420
Qy 421 LGAPRYQHIGLVAMFRONTGMWESNANVKTQIGAYFGASCLSDVDVDSNGSDTLVLIGAP 480
Db 421 LGAPRYQHIGLVAMFRONTGMWESNANVKTQIGAYFGASCLSDVDVDSNGSDTLVLIGAP 480
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Db 481 HYYETRGQGVSVCPPLRGQRARWQCDVLYGEGQOPWGRFGAALTIVLGDVNGDKLTDVA 540
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Db 540 ICAPGEENRGAVALPHGTSGSGISPSHSORITAGSKLSPRLQYFGQSLSGGDLTMDGLV 600
Qy 601 DLTGVAQGHVLLLRQPVLRVKAIMEFNPREVARNVFECDQVVRKEAGEVRVCLHVQK 660
Db 600 DLTGVAQGHVLLLRQPVLRVKAIMEFNPREVARNVFECDQVVRKEAGEVRVCLHVQK 660
Qy 661 STRDLRREGQIOSVTVYDIALDSGRPHRAVNETKNSTRTOVLGLTQTCETLKLQLP 720
Db 660 NTKDLRREGQIOSVTVYDIALDSGRPHRAVNETKNSTRTOVLGLTQTCETLKLQLP 720
Qy 721 NCIEDPVPIVLRNFSVGTPLSAGNLRPLVLAEDAQLFTALPFEKNCNDNICODD 780
Db 720 DCVDSVSPILIRLNTLVGEPFRSGNLRPLVLAEDAQLFTALPFEKNCNDNICODD 780
Qy 781 LSITFSFMSLCLVVGGRPFENVTVRNDGSDSYRTQVTFPFLDLSYRKVSTLQNRS 840
Db 780 LSITFSFMSLCLVVGGRPFENVTVRNDGSDSYRTQVTFPFLDLSYRKVSTLQNRS 840
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Db 840 KKPWFVKAPESSSSSEHGALKSTTWINIHPIFPANSEVTFNITFDVDSKASLGKLLK 899
Qy 900 ANVTSENMPRTNKTETFOLELVKAVVMVTVSHGVSTKYNFTASENTRVMQHOXOVS 959
Db 900 ALVASENNMSRTHKTKFOLELVKAVVMVTVSHGVSTKYNFTASENTRVMQHOXOVS 959
Qy 960 NLGQSLPISLVFLVPLRNQVNIWDRPOVTFSENLSSCTCHTKERLPSSDSEFLAIRKAP 1019
Db 960 NLGQSLPISLVFLVPLRNQVNIWDRPOVTFSENLSSCTCHTKERLPSSDSEFLAIRKAP 1019
Qy 1020 VVNCISVACQRIQCDIPFGIOEEFNATLKNLSFDWYIKTSHNHLIVSTABEILFNDVS 1079
Db 1020 VVNCISVACQRIQCDIPFGIOEEFNATLKNLSFDWYIKTSHNHLIVSTABEILFNDVS 1079
Qy 1080 FTLLPQGFVFSOTETKVEPEVNPPLIVGSSVGLLALITAAALYKLGPFKROVK 1139
Db 1080 FTLLPQGFVFSOTETKVEPEVNPPLIVGSSVGLLALITAAALYKLGPFKROVK 1139
Qy 1140 DMWSEGGPPGABPQ 1153
Db 1140 DMWSEGGPPGABPQ 1153
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RESULT 3

Q9J130

ID Q9J130 PRELIMINARY; PRT; 1151 AA.

AC Q9J130;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Integrin beta 2 alpha subunit.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

NCBI_TaxID=10116;

Sequence from N.A.
Fathallah D.M. Sr., Zeria K. Jr.;
Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
-1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
-1- SIMILARITY: Belongs to the integrin alpha chain family.
EMBL; AF268593; AAF81280.1; -.
HSP; P11215; 1BHQ.
GO; GO:0008305; C:intrig complex; IEA.
GO; GO:0007160; P:cell-matrix adhesion; IEA.
GO; GO:0007229; P:intrig-mediated signalling pathway; IEA.
InterPro; IPR000413; Intrig_alpha.
InterPro; IPR002035; VWF_A.
Pfam; PF01839; FG-GAP; 2.
Pfam; PF00092; VWA; 1.
PRINTS; PR01185; INTEGRINA.
PRINTS; PR00453; VWFADOMAIN.
SMART; SM00191; Intr_alpha; 5.
SMART; SM00327; VWA; 1.
PROSITE; PS00242; INTEGRIN_ALPHA; 1.
PROSITE; PS0234; VWFA; 1.
Cell adhesion; Integrin; Transmembrane.
SEQUENCE 1151 AA; 126943 MW; 8F785695D4074CA5 CRC64;

Query Match 74.9%; Score 4456; DB 2; Length 1151;
Best Local Similarity 73.4%; Pred. No. 1.8e-284;
Matches 846; Conservative 145; Mismatches 160; Indels 2; Gaps 2;

Qy 1 MALRVLLTALTLCGFNLDTENMTFOENARGQSVVQLQGSVAVVVCAPQEIIVAAQOR 60
Db 1 MTLKLLVLTALTLCGFNLDTENMTFOENARGQSVVQLQGSVAVVVCAPQEIIVAAQOR 60
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Db 121 GLCYFLGNLRLKQKPFPEALRGCPQEDSDIAFLIDGSGSIIPHFRMKFVSTVMEQL 180
Qy 181 KSKTLPMSLMQYSEFRTHFTKFPQNNPNRSLVKPIITGLGRTHATGIRKVVRELEN 240
Db 181 KSKTLPMSLMQYSEFRTHFTKFPQNNPNRSLVKPIITGLGRTHATGIRKVVRELEN 240
Qy 241 ITNGARKNAKILVITDGEKFGDPLGYEDVPEADREGVIRYVIGVGFADFRSEKSRQL 300
Db 241 ITNGARKNAKILVITDGEKFGDPLGYEDVPEADREGVIRYVIGVGFADFRSEKSRQL 300
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Qy 361 SNGPLLSVGSVDWAGGVFLYTSKEKSTFINMTRVDSMDNDAYLGYAAAILLRNRVQSLV 420
Db 361 SNGPLLSVGSVDWAGGVFLYTSKDKVTFINTRVDSMDNDAYLGYAAAILLRNRVQSLV 420
Qy 421 LGAPRYQHIGLVAMFRONTGMWESNANVKTQIGAYFGASCLSDVDVDSNGSDTLVLIGAP 480
Db 421 LGAPRYQHIGLVAMFRONTGMWESNANVKTQIGAYFGASCLSDVDVDSNGSDTLVLIGAP 480
Qy 481 HYYETRGQGVSVCPPLRGQRARWQCDVLYGEGQOPWGRFGAALTIVLGDVNGDKLTDVA 540
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Qy 541 ICAPGEENRGAVALPHGTSGSGISPSHSORITAGSKLSPRLQYFGQSLSGGDLTMDGLV 600
Db 540 ICAPGEENRGAVALPHGTSGSGISPSHSORITAGSKLSPRLQYFGQSLSGGDLTMDGLV 600
Qy 601 DLTGVAQGHVLLLRQPVLRVKAIMEFNPREVARNVFECDQVVRKEAGEVRVCLHVQK 660
Db 600 DLTGVAQGHVLLLRQPVLRVKAIMEFNPREVARNVFECDQVVRKEAGEVRVCLHVQK 660

DT 01-FEB-1991 (Rel. 17, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Integrin alpha-X precursor (Leukocyte adhesion glycoprotein p150,95
 DE alpha chain) (Leukocyte adhesion receptor p150,95) (CD11c) (Lieu M5).
 GN Name=ITGAX; Synonyms=CD11c;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=8816645; PubMed=3327687;
 RX Corbi A.L., Miller L.J., O'Connor K., Larson R.S., Springer T.A.;
 RA "cDNA cloning and complete primary structure of the alpha subunit of a
 RT leukocyte adhesion glycoprotein, p150,95.";
 RL EMBO J. 6:4023-4028(1987).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=90153906; PubMed=2303426;
 RX Corbi A.L., Garcia-Aguilar J., Springer T.A.;
 RA "Genomic structure of an integrin alpha subunit, the leukocyte p150,95
 RT molecule.";
 RL J. Biol. Chem. 265:2782-2788(1990).
 RN [3]
 RN ERRATUM.
 RP Corbi A.L., Garcia-Aguilar J., Springer T.A.;
 RL J. Biol. Chem. 265:12750-12751(1990).
 RN [4]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Blood;
 RX MEDLINE=2338257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.L., Feingold E.A., Grouse L.H., Dexe J.G.,
 RA Strausberg R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan J., Moore I., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marasina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RN SEQUENCE OF 20-43.
 RP MEDLINE=87167596; PubMed=3549901;
 RX Miller L.J., Wiebe M., Springer T.A.;
 RA "Purification and alpha subunit N-terminal sequences of human Mac-1
 RT and p150,95 leukocyte adhesion proteins.";
 RL J. Immunol. 138:2381-2383(1987).
 CC -!- FUNCTION: Integrin alpha-X/beta-2 is a receptor for fibrinogen. It
 CC recognizes the sequence G-P-R in fibrinogen. It mediates cell-cell
 CC interaction in monocyte inflammatory responses. It is especially
 CC important in monocyte adhesion and chemotaxis.
 CC -!- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-X
 CC associates with beta-2.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Predominantly expressed in monocytes and
 CC granulocytes.
 CC -!- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins
 CC with I-domains do not undergo protease cleavage.
 CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
 CC -!- SIMILARITY: Contains 7 FG-GAP repeats.
 CC -!- SIMILARITY: Contains 1 VWFA domain.

-!- DATABASE: NAME=PROW; NOTE=CD guide CD11c entry;
 WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd11c.htm".

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 or send an email to license@isb-sib.ch).

 EMBL; M81695; AAA59180.1; -;
 EMBL; M29165; -; NOT ANNOTATED CDS.
 EMBL; M29487; AAA51620.1; ALT SEQ.
 EMBL; M29482; AAA51620.1; JOINED.
 EMBL; M29483; AAA51620.1; JOINED.
 EMBL; M29484; AAA51620.1; JOINED.
 EMBL; M29485; AAA51620.1; JOINED.
 EMBL; M29486; AAA51620.1; JOINED.
 EMBL; BC038237; AAA38237.1; -;
 PIR; A36584; RWHU1C.
 PDB; 1N3Y; X-ray; A=141-338.
 Genew; HGNC:6152; ITGAX.
 MIM; 151510; -;
 GO; GO:0008305; C:integrin complex; TAS.
 GO; GO:0004872; F:receptor activity; TAS.
 GO; GO:0007155; P:cell adhesion; TAS.
 GO; GO:0009887; P:organogenesis; TAS.
 InterPro; IPR000413; Integrin_alpha.
 InterPro; IPR002035; VWF_A.
 Pfam; PF01839; FG-GAP; 3.
 Pfam; PF00357; Integrin_alpha; 1.
 Pfam; PF00092; VWFA; 1.
 PRINTS; PR01185; INTEGRINA.
 PRINTS; PR00453; WFPADOMAIN.
 SMART; SM00191; Int_alpha; 5.
 SMART; SM00327; VWFA; 1.
 PROSITE; PS00242; INTEGRIN_ALPHA; 1.
 PROSITE; PS50334; VWFA; 1.
 3D-structure; Calcium; Cell adhesion; Direct protein sequencing;
 Glycoprotein; Integrin; Magnesium; Polymorphism; Receptor; Repeat;
 Signal; Transmembrane.
 SIGNAL 1 19
 CHAIN 20 1163 Integrin alpha-X.
 DOMAIN 20 1107 Extracellular (Potential).
 TRANSMEM 1108 1128 Potential.
 DOMAIN 1129 1163 Cytoplasmic (Potential).
 REPEAT 34 87 FG-GAP 1.
 REPEAT 88 ? FG-GAP 2.
 DOMAIN 165 351 VWFA.
 REPEAT 401 401 FG-GAP 3.
 REPEAT 402 453 FG-GAP 4.
 REPEAT 455 517 FG-GAP 5.
 REPEAT 518 576 FG-GAP 6.
 REPEAT 581 633 FG-GAP 7.
 CA_BIND 466 474 Potential.
 CA_BIND 530 538 Potential.
 CA_BIND 593 601 Potential.
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 DISULFID 108 126 By similarity.
 DISULFID 655 712 By similarity.
 DISULFID 771 777 By similarity.
 DISULFID 848 863 By similarity.
 DISULFID 998 1022 By similarity.
 DISULFID 1027 1032 By similarity.
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 CARBOHYD 89 89 N-linked (GlcNAc...) (Potential).
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 CARBOHYD 697 697 N-linked (GlcNAc...) (Potential).
 CARBOHYD 735 735 N-linked (GlcNAc...) (Potential).
 CARBOHYD 899 899 N-linked (GlcNAc...) (Potential).
 CARBOHYD 939 939 N-linked (GlcNAc...) (Potential).

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FT CARBOHYD 1050 1050 N-linked (GlcNAc...) (Potential).
FT VARIANT 48 48 W -> R (in dbSNP:11574633).
FT 1050 1050 /FTId=VAR_018672.
FT CONFLICT 209 209 T -> S (in Ref. 4).
FT CONFLICT 251 251 T -> A (in Ref. 4).
FT CONFLICT 469 469 T -> S (in Ref. 4).
FT CONFLICT 490 490 G -> A (in Ref. 2).
FT CONFLICT 547 547 E -> K (in Ref. 4).
FT CONFLICT 756 756 D -> L (in Ref. 4).
FT CONFLICT 819 819 I -> V (in Ref. 1).
FT CONFLICT 1161 1163 SEK -> TPHYQDNV (in Ref. 4).
FT STRAND 150 157
FT TURN 160 161
FT TURN 164 178
FT TURN 179 180
FT TURN 183 185
FT TURN 186 193
FT STRAND 197 201
FT HELIX 203 208
FT HELIX 212 216
FT TURN 217 218
FT STRAND 226 226
FT HELIX 228 236
FT TURN 237 240
FT HELIX 242 244
FT TURN 245 245
FT TURN 248 249
FT STRAND 251 258
FT STRAND 263 263
FT HELIX 269 278
FT TURN 279 280
FT STRAND 282 288
FT HELIX 290 293
FT TURN 296 297
FT HELIX 298 304
FT HELIX 310 312
FT STRAND 313 316
FT HELIX 319 325
FT HELIX 326 334
FT TURN 335 335
SQ SEQUENCE 1163 AA; 127886 MW; 83658A13B5C5DE8F CRC64;

Query Match 59.0%; Score 3510; DB 1; Length 1163;
Best Local Similarity 61.3%; Pred. No. 4.3e-222;
Matches 700; Conservative 139; Mismatches 296; Indels 6; Gaps 4;

QY 5 VLLLTALTLCHGFNLDTENAMTFQENARGFGQSVVQLQGRVYVVCAPQEIIVAANQSGSLY 64
DB 8 LLLFTALATSLGFLNLDTBELTAFRVDSAGFGDSVVQYANSWVVGAPQKITAANQTGGLY 67

QY 65 QCDYSTGSCPTRLQVPVEAVNMISLGLSLAATSPPLQACGPTVHQTCSNTYVKGLCF 124
DB 68 QCGYSTGACEPLGLQVPEAVNMISLGLSLASTTSPSLLACGPTVHCEGGRNWLTLGLCF 127

QY 125 LFGSNLRQPKFPKFPALRGCPQEDSDIAPLDGSGSIIPHDFRMRKEFVSTVMEQLKSKS 184
DB 128 LLGPT--QLTQRLPVSRQECPRQEQDIIVFLDGGSGSISSRNFAWMNFVRAVISQFORPS 185

QY 185 TLPSLMQYSEERIHFTKEFQNNPNRSLVKPITQLGRTHATGIRKVRLENITNG 244
DB 186 TQFLMQSNKFPQTHFTFEEFRRTSNPLSLASVHQLQGTYYTATAIQNVVHRLPHASYG 245

QY 245 ARKNAFKILVITDGEKFGDPLGYEDVTPADREGVIRYVIGVDAPFRSEKSRQBLNTIA 304
DB 246 ARRDATKILVITDGEKFGDPLGYEDVTPADREGVIRYVIGVDAPFRSEKSRQBLNTIA 305

QY 305 SKPPRDHVPQNNFALKTIQNLREKXPAIEGTGTGSSSFEHMSQEGFSAATISNGP 364
DB 306 SKPSQEHIFKVEDFDALXDIQNLKEKIFAIEGTETTSSTSSFELEMAQEGFSAVFTPDGP 365

QY 365 LLSTVGSVDWAGGVFLYTSKEKSTFINTRVDSQNDMDAYLGVAAAILRNVSQSLVGLAP 424
DB 366 VLGAVGSTWGGAFLLYPNMSPTFINMSQENVDNRDSYLGYSTELALWKGVQSLVLGAP 425
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QY 425 RYOHITGLVAMPRQNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDVLVLIGAPHYYE 484
DB 426 RYHGTGKAVITQVSRQRMKAEVTGTQIGSYFGASLCSVDVDTGSTDVLVLIGAPHYYE 485

QY 485 QTRGGQSVSVCLPRGORARWQCDVLYGEOQOPWGRFGAALTVLGDVNGDKLITDVAIGAP 544
DB 486 QTRGGQSVSVCLPRGWR--RWCDAVLYGEOQHPWGRFGAALTVLGDVNGDKLITDVAIGAP 544

QY 545 GEEDNRGAVYLPFGTSGSGISPSHSQRIAGSKLAPRLQYFQGSLSGGQDLTWGDLVDLTV 604
DB 545 GEEENRGAVYLPFGHVLGSPISPSHSQRIAGSKLAPRLQYFQGSLSGGQDLTWGDLVDLTV 604

QY 605 GAQGHVLLLRQSVPLRVKAIIMEENPREVARNVFEENDOVVKGEAGEVRCVCLHWOKSTRD 664
DB 605 GARGQVLLLRTPVLWVGVSQGFPAEIPRFAFECREQVSEQTUVQSNICLIYIDKRSKN 664

QY 665 RLREGQIQSVVYTDIALDSGRPHSAFVNETKNSRTRQTVLGLTQTCTETLKLQLPNCIE 724
DB 665 LLGSRDLQSSVTLDALDPGRLSPRATFQETKNRSLSRVRLGLKAHCENFLLPLSCVE 724

QY 725 DPVSPVLRLNPSLVGTPLSAFGNLRPVLAEDAQRLFTALPFPKNCNDNICODDLSIT 784
DB 725 DSVTPITLRLNFTLVGKPLAFRLNLRPLMAADAQRYFTASLPFEKNCGADHICQDNLGIS 784

QY 785 FSPMSLDCLVVGGPREFNVTVRNDGSDSYRTQVTRPFPPLDLSYRKVSTLQNRQSRSW 844
DB 785 FSPFLKSLLVGSLNLELNAEVMVWNGDSDSYRTQVTRPFPFPAGLSYRYVAEGQKQQLRSL 844

QY 845 RLACESASTEVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLKANVTS 904
DB 845 HLTCDSPVG--SQGTWSTSCRINHLIFRGAQITFLATFDVSPKAVLGDRLLLTANVSS 902

QY 905 ENNMPRTNKTFFOLELPVKYAVYVWVTHSGVSTKYLNFTAS--ENTSRVMOHQYQVSNLQ 963
DB 903 ENNTPRTSKTFFOLELPVKYAVYVWVTHSGVSTKYLNFTAS--ENTSRVMOHQYQVSNLQ 962

QY 964 RSLPISLVFLVPLRLNQTIVWDRPQVTFPNSLSTCTCHKRLPSHSDFLAELRKPVVNC 1023
DB 963 RDLPVSNFVWVPELVNQAEMVMDVEVSHPPQPSLRCSSEKIAPASDFLAHIQKNPVLDC 1022

QY 1024 SIACVQRIQCDIPFFGIQEFNATLKNLSFDWYKITSNHNLLIVSTAEILPNDVSFTLL 1083
DB 1023 SIAGCLPRCDVPVSFQSELDFTLKGNSLFGWRQILQKKVSVVVAIEITFDTSVYSQL 1082

QY 1084 PQGAFVRSOTETKVEPEVPEVNPPLIVGSSVGGLLALITALYKLGFKRQYKQVMS 1143
DB 1083 PQGAFVRSOTETKVEPEVPEVNPPLIVGSSVGGLLALITALYKLGFKRQYKQVMS 1142

QY 1144 E 1144
DB 1143 E 1143
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RESULT 6

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ITAD HUMAN
ID ITAD HUMAN STANDARD; PRU; 1162 AA.
AC Q13349; Q15575; Q15576.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Integrin alpha-D precursor (Leukointegrin alpha D) (CD11d) (ADB2).
GN Name=ITGAD;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Splice;
RX MEDLINE=961111956; PubMed=8777714;
RA Van der Vliet H., Le Trong H., Wood C.L., Moore P.F., St John T.,
RA Staunton D.E., Gallatin W.M.;
```

RT "A novel leukointegrin, alpha d beta 2, binds preferentially to IGAM-
 RL 3.",
 RL Immunity 3:683-690(1995).
 RN [2]
 RP SEQUENCE OF 1-235 FROM N.A.
 RX MEDLINE=20187620; PubMed=10722744;
 RA Noti J.D., Johnson A.K., Dillon J.D.;
 RT "Structural and functional characterization of the leukocyte integrin
 RL gene Cld1. Essential role of Sp1 and Sp3."
 RL J. Biol. Chem. 275:8959-8969(2000).
 RN [3]
 RP SEQUENCE OF 467-537; 571-602; 633-666; 788-834 AND 910-1125 FROM N.A.
 RX MEDLINE=96257236; PubMed=8666289;
 RA Wong D.A., Davis E.M., LeBeau M., Springer T.A.;
 RT "Cloning and chromosomal localization of a novel gene-encoding a human
 RL beta 2-integrin alpha subunit."
 RL Gene 171:291-294(1996).
 RN [4]
 RP INTERACTION WITH VCAM1.
 RX MEDLINE=99059842; PubMed=9841932;
 RA Grayson M.H., Van der Vieren M., Sterbinsky S.A., Michael Gallatin W.,
 Hoffman P.A., Staunton D.E., Bochner B.S.;
 RT "alpha2beta2 integrin is expressed on human eosinophils and functions
 RL as an alternative ligand for vascular cell adhesion molecule 1 (VCAM-
 RL 1)."
 RL J. Exp. Med. 188:2187-2191(1998).
 RN [5]
 RP INTERACTION WITH VCAM1.
 RX MEDLINE=99370002; PubMed=10438935;
 RA Van der Vieren M., Crowe D.T., Hoekstra D., Vazquez R., Hoffman P.A.,
 Grayson M.H., Bochner B.S., Gallatin W.M., Staunton D.E.;
 RT "The leukocyte integrin alpha D beta 2 binds VCAM-1: evidence for a
 RL binding interface between I domain and VCAM-1."
 RL J. Immunol. 163:1984-1990(1999).
 CC -!- FUNCTION: Integrin alpha-D/beta-2 is a receptor for ICAM3 and
 CC VCAM1. May play a role in the atherosclerotic process such as
 CC clearing lipoproteins from plaques and in phagocytosis of blood-
 CC borne pathogens, particulate matter, and senescent erythrocytes
 CC from the blood.
 CC -!- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-D
 CC associates with beta-2.
 CC -!- SURCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed moderately on myelomonocytic cell
 CC lines and subsets of peripheral blood leukocytes and strongly on
 CC tissue-specialized cells, including macrophages foam cells within
 CC atherosclerotic plaques, and on splenic red pulp macrophages.
 CC -!- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins
 CC with I-domains do not undergo protease cleavage.
 CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
 CC -!- SIMILARITY: Contains 7 FG-GAP repeats.
 CC -!- SIMILARITY: Contains 1 VWFA domain.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in 'no way
 CC modified and this statement is not removed. Usage by and for commercial
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 CC
 CC -----
 DR EMBL; U37028; AAB38547.1; -;
 DR EMBL; U40274; AAB60634.1; -;
 DR EMBL; U40275; AAB60635.1; -;
 DR EMBL; U40276; AAB60636.1; -;
 DR EMBL; U40277; AAB60637.1; -;
 DR EMBL; U40279; AAB60638.1; -;
 DR EMBL; U40278; AAB60638.1; JOINED.
 DR EMBL; AF187881; AAF62875.1; -;
 DR HSSP; P11215; 1BHQ.
 DR Genew; HGNC:6146; ITCAD.
 DR MIM; 602453; -;
 DR GO; GO:0008305; C:integrin complex; TAS.
 DR GO; GO:0016337; P:cell-cell adhesion; NAS.

DR GO; GO:0007160; P:cell-matrix adhesion; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR000413; Integrin_alpha.
 DR InterPro; IPR002035; VWF A.
 DR Pfam; PF01839; FG-GAP; 3_
 DR Pfam; PF00357; Integrin_alpha; 1.
 DR Pfam; PF00092; VWFA; 1.
 DR PRINTS; PR01185; INTEGRINA.
 DR PRINTS; PR00453; VWFADOMAIN.
 DR SMART; SM00191; Int_alpha; 5.
 DR SMART; SM00327; VWFA; 1.
 DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.
 DR PROSITE; PS02334; VWFA; 1.
 DR Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
 KW Repeat; Signal; Transmembrane.
 FT SIGNAL 1 17 Potential.
 FT CHAIN 18 1162 Integrin alpha-D.
 FT DOMAIN 18 1100 Extracellular (Potential).
 FT TRANSMEM 1101 1121 Potential.
 FT DOMAIN 1122 1162 Cytoplasmic (Potential).
 FT REPEAT 32 85 FG-GAP 1.
 FT REPEAT 86 ? FG-GAP 2.
 FT DOMAIN 150 332 VWFA.
 FT REPEAT 350 400 FG-GAP 3.
 FT REPEAT 401 452 FG-GAP 4.
 FT REPEAT 454 516 FG-GAP 5.
 FT REPEAT 518 576 FG-GAP 6.
 FT REPEAT 581 633 FG-GAP 7.
 FT CA_BIND 465 473 Potential.
 FT CA_BIND 530 538 Potential.
 FT CA_BIND 593 601 Potential.
 FT SITE 1127 1131 GFFKR motif.
 FT DISULFID 67 74 By similarity.
 FT DISULFID 106 124 By similarity.
 FT DISULFID 655 710 By similarity.
 FT DISULFID 769 775 By similarity.
 FT DISULFID 846 861 By similarity.
 FT DISULFID 994 1018 By similarity.
 FT DISULFID 1023 1028 By similarity.
 FT CARBOHYD 59 59 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 87 87 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 99 99 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 391 391 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 691 691 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 733 733 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 873 873 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 957 957 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 1046 1046 N-linked (GlcNAc...) (potential).
 FT CONFLICT 500 500 Missing (in Ref. 2).
 FT CONFLICT 515 518 GHPW -> ATP (in Ref. 2).
 FT CONFLICT 825 825 L -> V (in Ref. 2).
 FT CONFLICT 984 984 V -> A (in Ref. 2).
 SQ SEQUENCE 1162 AA; 126885 MW; F296A1A35455D77D CRC64;
 Query Match 58.0%; Score 3452; DB 1; Length 1162;
 Best Local Similarity 59.9%; Pred. No. 2.9e-218;
 Matches 683; Conservative 163; Mismatches 287; Indels 8; Gaps 6;
 QY 5 VLLLTALTLCHGNLDLTENAMTFQENARGFGQSVVVLQSGSRVVGAPQEIIVAAVNGSGLY 64
 DB 6 VLLLSVLASYHGNLVDVEEPTFOEDAGGQSVVVGFGSRLVVGAPLEVVAAVNGTGRLY 65
 QY 65 QCDYSTGSCBPIRLQVPVEAVNMSLGLSLAATTSPPOLLACGPTVHQTCSNTYVKGKLCF 124
 DB 66 DCAATGWCQPIPLHIREAVNMSLGLTLASTNGSRLACGPTLHRVCGENSYSKGSCL 125
 QY 125 LFGSNLRQOPKPFALRGCPQEDSDIAFLIDGSGSIIPHFRMKFVFTVWEQKKSK 184
 DB 126 LLGSRW-EIIQTVPDATPECPHQEMDIVFLIDGSGSIDQNDPNQMKGFVQAVMGQFEGD 184
 QY 185 TLFSLMOYSEFRHTFTKEFQNNPNRSLVKPTQLGRTHATGIRKVVRELINING 244
 DB 185 TLFALMOYSNLLKTHFTFTQFRTSPSQOQLVDPIVLQKGLTFTATGILTFTVTLPHRNG 244

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QY 245 ARKNAFKILVITDGEKFGDPLGYEDVPEADREGVIRYVIGVDAFRSEKSRQBLNTIA 304
DB 245 ARKSAKKILVITDGKQKDPLEYSVDVPEAKAGIIRYAVIGVGHAFQGPAPARQELNTIS 304
QY 305 SKPPRDHVPQVNNFALKTIQNLREKKAIPABGTGTGSSSSPEHEMSQEGFSAATSNP 364
DB 305 SAPPQDHFVKNFNAALGSIQKQLEKIYAVGTQSRASSSPQHEMSQEGFSTALTMGL 364
QY 365 LSTVGSYDWDAGVFLYTSKEKSTFINTRVDSMDNDAYLGAALILRNVRQSVLIGAP 424
DB 365 FUGAVGSFSWGGATFLPPNMSPTFINMSQENVDNRDYLGYSTELALWKGVQNLVLGAP 424
QY 425 RYQHIGLVAMFRQNTGMWESNANVKTQIGAYFGASLCSVDVDSNGSTDVLILGAPHYIE 484
DB 425 RYQHTGKAVIFQVSRQWRKKAETVGTQIGSYFGASLCSVDVDSNGSTDVLILGAPHYIE 484
QY 485 QTRGGQVSVCPPLPRGORARWQCDVLYGEGQPGWRFGAALTVLGDVNGDKLTVDAIGAP 544
DB 485 QTRGGQVSVCPPLPRGORVQWQCDVLRGEQHPWGRFGAALTVLGDVNEKDLIDVAIGAP 544
QY 545 GEEDNRGAVYLFPHGTSGSISPSHSORTAGSKLSPLOYFGOSLGGODLTMGLVDTLV 604
DB 545 GEQENRGAVYLFPHGASEGISPSHSORTASSQLSPRLQYFGQALSGGQDLTQDGLMDLAV 604
QY 605 GAQGHVLLRSQPLVLRKALMEFNREVARNVFECDQVVGKEAGEVRVCLVHVKSTRD 664
DB 605 GARGQVLLRSPLVLRKGVWRFSPVEVAKAYRCWEKPSALEAGDATVCLTIQKSSLD 664
QY 665 RLREGQISVTVYDIALDSGRPHSRVAVNETKSTRQTVLGLPQTCTETKLQLPNCIE 724
DB 665 QL--GDIQSSVRFDLALDPGRULTSRAIFNETKNPTLTRKTLGLIHCECTKLKLLPDCE 722
QY 725 DPVSPILVRLNPLSVGTPLSARGNLRPVLAEDAQRLFTALPFEKNCNGNDNICQDLSIT 784
DB 723 DVVSPILILHNLFSLVREPIPSQNLRPVLAVGSDQLFTASLPFEKNCQDGLCEGDLGV 782
QY 785 F5FMSLDCLVGGPREFNVTVTRNDGEDSVRTQVTFPPFLDLSYRKVSTLQNRQSRW 844
DB 783 L5FSGQLTLTVGSSLELVNVTVMNAGEDSYGTVVSLYYPAGLSHRVSGAQPHQSAL 842
QY 845 RLACASASTVSGALKSTSCINHIPIIPENSEVTNITFDVDSKASLGNKLLKANVTS 904
DB 843 RLACETV--PTEDEG--LRSSRCVNHPIFHEGNGTFTVTFDVSYKATLGDRLMFASS 900
QY 905 ENNMPTNKTEFQLELPVKYAVVMVTSHGVSSTKYNL--TASENTRVMQHOYQVNLGQ 963
DB 901 ENNKASSKATFQLELPVKYAVVIMISRQESTKYFNATSEKQKQKAEHRVYNNLSQ 960
QY 964 RSLPLSLVFLVRLNQTVINDRPQVTFSENLSSTCHTKERLPSHDSFLAELRKAPVVC 1023
DB 961 RDLAISINFWPVLNGVAVNDVMEAPSQSL--PCVSEKPPQHSDFLTQISRSPMLDC 1018
QY 1024 SIACVQRCQDIPFGIIEFNATLKNLSFDWYIKTSHNHLIIVSTAEILFNDSVFTLL 1083
DB 1019 SIADCLQRCDFPSVSGEELDTLKNLSFGWVRETIQKVLVVSVAEITFDTYSVQL 1078
QY 1084 PQGAFVFSOTETKVEPEVNPPLIYGVSSVGGILLALITAAALYKLGFFKRYQKMS 1143
DB 1079 PQGAFMRQAEQMWLEEDVEVNAIPIINGSSVGALLLALITATLYKLGFFKRYKEMLE 1138
QY 1144 E 1144
DB 1139 D 1139
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RESULT 7

Q6KAS4

ID Q6KAS4

AC Q6KAS4

DT 05-JUL-2004

DT 05-JUL-2004

DT 05-JUL-2004

PRELIMINARY; PRT; 1188 AA.

(TRENBLrel. 27, Created)

(TRENBLrel. 27, Last sequence update)

(TRENBLrel. 27, Last annotation update)

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DE MFLJ00114 protein (Fragment).
GN Name=mFLJ00114;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Suga Y., Kitamura H., Nakagawa T., Nagase T., Ohara O., Koga H.;
RT "Prediction of the Coding Sequences of Mouse Homologues of FLJ Genes:
RT The Complete Nucleotide Sequences of 110 Mouse FLJ-Homologous cDNAs
RT Identified by Screening of Terminal Sequences of cDNA Clones Randomly
RT Sampled from Size-Fractionated Libraries.";
RL DNA Res. 11:167-180(2004).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
DR EMBL; AK131133; BAD31383.1; -.
DR GO; GO:0009897; C:external side of plasma membrane; IDA.
DR InterPro; IPR000413; Integrin_alpha.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF01839; FG-GAP; 3.
DR Pfam; PF00357; Integrin_alpha; 1.
DR Pfam; PF00092; VWA; 1.
DR PRINTS; PR01185; INTEGRIN.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00191; Int_alpha; 5.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS00242; INTEGRIN_ALPHA; UNKNOWN_1.
DR PROSITE; PS50234; VWFA; 1.
DR Cell adhesion; Integrin; Transmembrane.
FT NON TER 1
SQ SEQUENCE 1188 AA; 131248 MW; B8D93107BDBB4178 CRC64;

Query Match 56.4%; Score 3358.5; DB 2; Length 1188;
Best Local Similarity 57.2%; Pred. No. 4.4e-212;
Matches 658; Conservative 167; Mismatches 307; Indels 19; Gaps 7;

QY 6 LLLTALTLCFGLNDTENAMTFQGNARFGQSVVQLQSGRVVVGAPQSIIVANORGSILYQ 65
DB 28 LLLGFGVSLGFLNDAEKPTFHMDGAEFGHSVLYQYDSSVWVGAPREIKATNQIGLYK 87
QY 66 CDYSTGSCPTLRQVPVEAVNMSLGLSLAATSPQLLACGPTVHQTSCENTYVKGCLFL 125
DB 88 CGYHTGNCPEISLPVPEAVNMSLGLSLAATNPSSLACGPTVHHTCRENIIYLTGLCFL 147
QY 126 FGSNLRQOPQFPALRGCPQEDSDIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKKSKT 185
DB 148 LSSSFKQS-QNFPYTAQCEPKQDQDIVFLIDGSGSISSTDPEKMLDFYKAVMSQLQRPST 206
QY 186 LFSLMQYSEBPIHPTKPEFONNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGA 245
DB 207 RFSLMQFSYPRVHFTNFNFISTSPSLDLSVQLRGYTTASAKHVIITELFTTQSGA 266
QY 246 RKNAFKILVITDGEKFGDPLGYEDVPEADREGVIRYVIGVDAFRSEKSRQBLNTIAS 305
DB 267 RQDATKVLIVITDGRKQGNLSYDSVIPMAEASIIRYAIGVGKAFYNEHSHKQELKATAS 326
QY 306 KPPRDHVPQVNNFALKTIQNLREKKAIPABGTGTGSSSSPEHEMSQEGFSAATSNP 365
DB 327 MPSEHYVFSVNFDAKDIEQLKEKIPABGTGTSPSSSTFELEMSQEGFSAVTPDGPV 386
QY 366 LSTVGSYDWDAGVFLYTSKEKSTFINTRVDSMDNDAYLGAALILRNVRQSVLIGAPR 425
DB 387 LGAVGSFSWGGATFLYPSNMRPTFINMSQENEDNRDAYLGYSTALAFWKGVHSLILGAPR 446
QY 426 YQHIGLVAMFRQNTGMWESNANVKTQIGAYFGASLCSVDVDSNGSTDVLILGAPHYIE 485
DB 447 HQHTGKVVIFQESRHRWRPKSEVRGTQIGSYFGASLCSVDMDRDSGLDVLIGVPHYIEH 506
QY 486 TRGGQVSVCPPLPRGORARWQCDVLYGEGQPGWRFGAALTVLGDVNGDKLTVDAIGAP 545
DB 507 TRGGQVSVCPMP-GVGRRWHCCTTLHGEQGHWPGRFGAALTVLGDVNGDSDLADVAIGAP 565
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QY 546 EDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGQDLTMDGLVDLTVG 605
DB 566 EENRGAVYIFHGASRQDIAPSPORISASQIPSRIOYFGQSLSGQDLTMDGLVDLAVG 625
QY 606 ACHVLLRSQPLRVKALMEPNPREVARNVPECNDQVVKGEAGEVRVCLHVQKSTRDR 665
DB 626 SKGRVLLLRTRILRVSPVHTTPAEISKSVECEQVAPBQTLSDATVCLHHSKPTQ 685
QY 666 LREGQIQSVVTVYDLALDSCGRPHSRVAFNETKNSRTRQTVLGTQTCETLKLQPLNCIED 725
DB 686 L--GDLRSTVTFDLALDHGRLSTRAIFKETKTRALTRVKTGLNKHCHESVKLLLPACVED 743
QY 726 PVSPIVLRNLSVLTGTPLSAFGNLRPVLAEADQRLFTALFPPEKNCNDNICQDDLSITF 785
DB 744 SVTPITLRNLSVLTGTPVPISSQLNQLPMLAVDDQTYFTASLPFEKNCADHICQDDLSVVF 803
QY 786 SFMSLDCLVVGPREFNVTVVRNDEGDSYRTQVTFPRLDLSYRKVSTLQ----- 836
DB 804 GFPDLKTLVVGSDLELVNVDVTSNDEGDSYGTVTLPVPGVLSFRVARGQVFLRKEDQ 863
QY 837 --NORSQSRWLACESASSTESVSGALKSTSCSINHPIPFENSEVTFNITFDVDSKASLGN 894
DB 864 QWRRGQSHLHLMCD--STPDRSQGLWSTSCSSRHVIFRGSGQMTFLVTFDVSFKAELED 921
QY 895 KULLKANVTSENNMPTNKTETFOLELPVKYAVYVMTSHGVSTKYLNFTASE-NTSRVWQ 953
DB 922 RLLLRARVGSNNVPGTPTTFOLELPVKYAVYVMTSHHDQTKYLNFTSEKETSVE 981
QY 954 HOYQVSNLQORSPLSLVPLVPLNQTVMWRPQVTFSENLSSTCHTKERLPSHSDFLA 1013
DB 982 HRFQVNNLQORDVPVSNFVWPIELKGEAV--TVMVSHPNQLTCYRNLKPTQDFLT 1040
QY 1014 ELRKAPVNCSTAVCQRIQCDDIPFGIOEFPNATLKGNSLFDWYIKTSHNHLIVSTAEI 1073
DB 1041 HMOKSPVLDCSIADCLHLRCDIPSLGILDELFLKGNLSFGWISQTLQKXVLLSEABI 1100
QY 1074 LFNDSVFTLLPGGAFVRQSTKVEPVPNPLPLIVGSSVGGILLIILAIITAYLXKGF 1133
DB 1101 TENTSYSQPLQGEAPFLRAQTKTVLEMYKVHPVPLIVGSSVGGILLIILAIITAYLXKGF 1160
QY 1134 FKROYKDMWSE 1144
DB 1161 FKROYKEMLEE 1171

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RESULT 8

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BAD21383 PRELIMINARY; PRT; 1188 AA.
AC BAD21383;
DT 01-JUN-2004 (TrEMBLrel. 27, Created)
DT 01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DE MFLJ00114 protein (Fragment).
GN MFLJ00114.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Saga Y., Kitamura H., Nakagawa T., Nagase T., Ohara O., Koga H.;
RT "Prediction of the Coding Sequences of Mouse Homologues of FLJ Gene:
RT The Complete Nucleotide Sequences of 110 Mouse FLJ-homologous cDNAs
RT Identified by Screening of Terminal sequences of cDNA Clones Randomly
RT Sampled from Size-Fractionated Libraries."
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK131133; BAD21383.1; --
FT NON TER 1
SQ SEQUENCE 1188 AA; 131248 MW; BBD93107BDBB4178 CRC64;

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Query Match

56.4%; Score 3358.5; DB 2; Length 1188;

```

Best Local Similarity 57.2%; Pred. No. 4.4e-212;
Matches 658; Conservative 167; Mismatches 307; Indels 19; Gaps 7;

QY 6 LLLTALTILCHGFNLPTENAMTFQENARGFQSVVLOGRQSVVVGAPQBIIVANRQGSLYQ 65
DB 28 LLLGLFVSCGLFNLDKPTFHMDGAFGHVSLQYDSSVWVVGAPKEIKATNQIGGLYK 87
QY 66 CDYSTGSECEPRLQVPVAVANMGLSLAANTSPOLLACGPTVHTQTSNTYVYVGLCPFL 125
DB 88 COYHTGNCCEPISLQVPPVAVANMGLSLAANTSPOLLACGPTVHTQTSNTYVYVGLCPFL 147
QY 126 FGSNLRQOPQKPFPEALRCGPQEDSDIAFLIDGSGSIIPHDPERMKEFVSTVMEQLKSKKT 185
DB 148 LSSSFQKS-QNPPTAQECQPDQDIVFLIDGSGSISSTDFEKLMDFFKAVMSQQRPT 206
QY 186 LFSLMQYSEERIHTPFKEFQNNPNRSLVKPITQLLGRTHITATGIRKVVRELFNITGA 245
DB 207 RFLSMQFSDYFRVHTFNNFISTSSPLSLDSVRQVGYTYTASAIKHVITELFTTQSCA 266
QY 246 RKNAPKILVITDGBKFGDPLGYEDVIEADREGVIRVIVGVGDAPFRSEKSEKOEINTAS 305
DB 267 RQDATKVLIVITDGRKQGDNLSDSVIPMAEASAIIRYAIQVGFKAFYNEHSHKQELKATAS 326
QY 306 KPPRDHVFQVNFALKTIONQREKXFAIEGTOTGSSSSPHEMSQEGFSAITSNGL 365
DB 327 MSHSYVFSVENFDKDIENQLEKEIFAIEGTETPSSSTPELEMSQEGFSAVTFDGPV 386
QY 366 LSTVGSYDQWAGVFLYTSKEKSTFINMTRVDSMDNDVLAAGAAIILNRVQSLVLGAPR 425
DB 387 LGAVGFSWAGVFLYPSNMRPTFINMSQENEDMDVLAAGAAIILNRVQSLVLGAPR 446
QY 426 YOHIGLVAMFQNTQWESNANVKTQIYAGFASLCSVDVDSNGSTDLVLIGAPHYEQ 485
DB 447 HOHTKGVVIFTQESHRWPKSEVRGTQISYFASLCSVDMDRDSGLDLVLIGAPHYEH 506
QY 486 TRGGQVSCPLPRQARAWQCDVLYGOGOPWGRFGAALTVLGVNVDGKLTDAVAGP 545
DB 507 TRGGQVSCPLPRQARAWQCDVLYGOGOPWGRFGAALTVLGVNVDGKLTDAVAGP 565
QY 546 BEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGQDLTMDGLVDLTVG 605
DB 566 EENRGAVYIFHGASRQDIAPSPORISASQIPSRIOYFGQSLSGQDLTMDGLVDLAVG 625
QY 606 ACHVLLRSQPLRVKALMEPNPREVARNVPECNDQVVKGEAGEVRVCLHVQKSTRDR 665
DB 626 SKGRVLLLRTRILRVSPVHTTPAEISKSVECEQVAPBQTLSDATVCLHHSKPTQ 685
QY 666 LREGQIQSVVTVYDLALDSCGRPHSRVAFNETKNSRTRQTVLGTQTCETLKLQPLNCIED 725
DB 686 L--GDLRSTVTFDLALDHGRLSTRAIFKETKTRALTRVKTGLNKHCHESVKLLLPACVED 743
QY 726 PVSPIVLRNLSVLTGTPLSAFGNLRPVLAEADQRLFTALFPPEKNCNDNICQDDLSITF 785
DB 744 SVTPITLRNLSVLTGTPVPISSQLNQLPMLAVDDQTYFTASLPFEKNCADHICQDDLSVVF 803
QY 786 SFMSLDCLVVGPREFNVTVVRNDEGDSYRTQVTFPRLDLSYRKVSTLQ----- 836
DB 804 GFPDLKTLVVGSDLELVNVDVTSNDEGDSYGTVTLPVPGVLSFRVARGQVFLRKEDQ 863
QY 837 --NORSQSRWLACESASSTESVSGALKSTSCSINHPIPFENSEVTFNITFDVDSKASLGN 894
DB 864 QWRRGQSHLHLMCD--STPDRSQGLWSTSCSSRHVIFRGSGQMTFLVTFDVSFKAELED 921
QY 895 KULLKANVTSENNMPTNKTETFOLELPVKYAVYVMTSHGVSTKYLNFTASE-NTSRVWQ 953
DB 922 RLLLRARVGSNNVPGTPTTFOLELPVKYAVYVMTSHHDQTKYLNFTSEKETSVE 981
QY 954 HOYQVSNLQORSPLSLVPLVPLNQTVMWRPQVTFSENLSSTCHTKERLPSHSDFLA 1013
DB 982 HRFQVNNLQORDVPVSNFVWPIELKGEAV--TVMVSHPNQLTCYRNLKPTQDFLT 1040
QY 1014 ELRKAPVNCSTAVCQRIQCDDIPFGIOEFPNATLKGNSLFDWYIKTSHNHLIVSTAEI 1073
DB 1041 HMOKSPVLDCSIADCLHLRCDIPSLGILDELFLKGNLSFGWISQTLQKXVLLSEABI 1100

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FT	DISULFID	842	858	By similarity.	
FT	DISULFID	994	1009	By similarity.	
FT	DISULFID	1017	1048	By similarity.	
FT	CARBOHYD	33	33	N-linked (GlcNAc. .)	(Potential).
FT	CARBOHYD	86	86	N-linked (GlcNAc. .)	(Potential).
FT	CARBOHYD	185	185	N-linked (GlcNAc. .)	(Potential).
FT	CARBOHYD	646	646	N-linked (GlcNAc. .)	(Potential).
FT	CARBOHYD	667	667	N-linked (GlcNAc. .)	(Potential).
FT	CARBOHYD	723	723	N-linked (GlcNAc. .)	(Potential).
FT	CARBOHYD	859	859	N-linked (GlcNAc. .)	(Potential).
FT	CARBOHYD	894	894	N-linked (GlcNAc. .)	(Potential).
FT	CARBOHYD	929	929	N-linked (GlcNAc. .)	(Potential).
FT	CARBOHYD	1056	1056	N-linked (GlcNAc. .)	(Potential).
FT	CARBOHYD	1067	1067	N-linked (GlcNAc. .)	(Potential).
SQ	SEQUENCE	1165 AA;	128725 MW;	DABBA3A3F1E1463CB CRC64;	
Query Match					26.6%; Score 1583; DB 1; Length 1165;
Best Local Similarity					34.8%; Pred. No. 4.8e-95;
Matches 417; Conservative 200; Mismatches 475; Indels 108; Gaps 34;					
QY	1	MALRVLLLTALTLL--CHGFNLDTENAMTFQENARG--FGQSVVQLQGSRVVVGAPQEIIVA	56		
DB	6	IVLRULLSGPFVPAPAWSNLDVRHVQNFSPFLAGRHFGYRVLQV--GNGVVVGAPSE---61			
QY	57	ANQRGLYQCDYSTGCEPIRLQVPVEAVNMISLGLSIAANTPPQALLACGPTVHQTCSEN	116		
DB	62	GNSMGNLYQCPETGDCPLPTLS--SNYTSKYLGMTLATDPTSDNLLACDPLGSLRTCDQN	119		
QY	117	TVYKGLCFGLFSGNLROOQPFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRMKERVSTV	176		
DB	120	IYLSGLCYLIHENLRGVLYQGHGYQECIKGNVDLVLFDFGSGMSLQODEFKIVDFPMKDV	179		
QY	177	MBQLKSKTFLSLMOYSEBFRIHFTKFBQNNPNPRSLVKPIPTQLLGRTHRTATGRKVVVR	236		
DB	180	MXKLSNSYQFAAVQPSYTFRTFTLDYIRKQDPDALLAGVKHMLLNTTCAINYVAK	239		
QY	237	ELFNTINGARKNAFKILVVITGEKFGPLGVEDVITPEADRGVIRVYIVGVGDAPRSEKS	296		
DB	240	EVFRPLDGLARPATKVLIIITDGEATD----EHNIDAA--KDIIRYIIGIKGNFKTKES	292		
QY	297	RQELNTIASKPRDHVQVNNFEALTIQNLREKXFALEGTTQSGSSSPEHEMSQEGRS	356		
DB	293	QBALHOFASKPVEEFVKIILDTFEKLKDLFTLQKLIYIEGTSKQDLTSFNMLSSSGIS	352		
QY	357	AAITSGNPLSTVSGVDAGGVF--LYTSKXKSTFINMTRVDSMDNDAIYLGAAA--ILLRN	414		
DB	353	ADLSEGHGVVAVGAKDWAGGLDLKADLKSSTFVNGEPLTVESRAGLYGYTVWLPSPRG	412		
QY	415	RVQSLVLGAPRYQHIGLVAMFRQ--NTGMWESNANVKGTOIGAYFASLCSVDVDSNGST	472		
DB	413	TMSLLATGAPRYQHVGRVLLFQPKRGKGPWSQIETDGIQIGSYFGGELCGVDVDRDGET	472		
QY	473	DLVILGAPHYEOTRGQSVCPPLPRGARWQCDALVLYGEOGPMGRFGAALTVLGDVN	532		
DB	473	ELLTLAALPYGEQGRGVFY---QKIQLEFQWSELQOETGYPLGRFGAALAAALTDIN	529		
QY	533	GDKLTDVAICAGEEDNRGAVLFIHGTSGSGSPSHSQRISAGLSKPRIQYFQSGLSGQ	592		
DB	530	GDELTDAVAGAPLEE--QGANVIFNQOG--GLSPRESQRIEGTQMSGIOWFGRSIHGVK	586		
QY	593	DLTMDGLVLTGVAQGHVLLLSQPVLRVKAIMEFNPVRVARNVFPCNDQVVKGEAG--E	651		
DB	587	DLGGDGLADVAVAGAQVIVLSRPPVDIITSVSFSPABIPVHEVECSYSTSNQKKEGVN	646		
QY	652	VRVCLHVQK--STRDLRGQTSVVTYDLADSGRPHSRVAFNEFNSRQTVQLGIT	709		
DB	647	LTVCFQVKSLIST-----FQHLVANVITYLQDGHRTSRGLFPFGKHLIGNTAVTPV-	701		
QY	710	QTCETLKLQLPNCIEDPVPVILRVNLSL---VGTPLS--AFGNLPVLAEDAQRLLFTAL	764		
DB	702	KSCFVFWFHPICIQDLISPINVLSYSLWEEGTFRDPRALDRDIPPIKPSPHLETKE	761		
QY	765	FPPEKNCNDNICQDLDLSTFSPMSLDCLVVGPGPREFNVTVTVRNDGEDSYRTQVTFPP	824		

RESULT 12

ITAL_HUMAN

ID ITAL_HUMAN STANDARD; PRT: 1170 AA.
AC P20701; O43746;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Integrin alpha-L precursor (Leukocyte adhesion glycoprotein LFA-1
DE chain) (CD11a).
GN Name=ITGAL; Synonyms=CD11A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE.
RX MEDLINE=89139587; PubMed=2537322;
RA Larson R.S., Corbi A.L., Berman L., Springer T.;
RT "Primary structure of the leukocyte function-associated molecule-1
RT alpha subunit: an integrin with an embedded domain defining a protein
RT superfamily.";
RL J. Cell Biol. 108:703-712(1989).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=99425270; PubMed=10493829;
RA Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R.,
RA Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L.,
RA Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S.,
RA Eichler E.B., Harris P.C., Venter J.C., Adams M.D.;
RT "Genome duplications and other features in 12 Mb of DNA sequence from
RT human chromosome 16p and 16q.";
RL Genomics 60:295-308(1999).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 153-335, AND REVISION TO 214.
RX MEDLINE=96036067; PubMed=7479767;
RA Qu A., Leahy D.J.;
RT "Crystal structure of the I-domain from the CD11a/CD18 (LFA-1, alpha L
RT beta 2) integrin.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:10277-10281(1995).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 153-335.
RX MEDLINE=96398682; PubMed=8805579;
RA Qu A., Leahy D.J.;
RT "The role of the divalent cation in the structure of the I domain from

Matches	409;	Conservative	211;	Mismatches	464;	Indels	110;	Gaps	38;
Qy	6	LLLTALTLCHGF	-----	NLDTEMATFQ	--ENARGEQSQSVVLQGSRRVVVGAPQEI	54			
Db	6	ITVAMALLSGFFPFA	PASSYNLNDRGARSFSP	PRAGRHFGRVQLQV	-GNGVIVGAPGE-	63			
Qy	55	VAANQRSLLYQCDY	STSCGPIRLQVPVEAVNMSLGLSLAATTSPP	OLLACGPVPHOTCS	114				
Db	64	--GNSTGSLYQCOS	GTGCHLPVTLR	-GSNTYSKYLGMTLATDPTDGSILACDPLGSR	120				
Qy	115	ENTVVGKLCFLFGS	NLR---	QQPQKPEALRGCPQEDSDIARLIDGSGSI	PHDFFRMK	170			
Db	121	QNTVYLSGLCYLFR	QNLQPMQLQGRPGQECIK	---NVDLVLFUDGSMQLDPDEFOKIL	176				
Qy	171	EFVSTVMEQLKSK	KTFLSLMOYSBEFRIHFTFKBFQNNPNRSLVAKP	ITOLLGRTHRTATG	230				
Db	177	DFMKDVMKKLSNT	SYQFAAQVFSYKTEPDFSDYVVRKDPDALLKHVKHMLLLTNT	FGA	236				
Qy	231	IRKVVRELFINI	TNGARKNAFKILVITDGEKFGDPLGYEDVI	PEADREGVIRYVIGVGD	290				
Db	237	INTVATVVFREL	GARDPATKVLIIITDGE	-ATDSGNIDAADK-----IIRVIIGTCKH	289				
Qy	291	PREKSRQELNT	ASKPDRHVFOVNNFEALKTIQNLREKXFAIEGTQ	TCSSSSPEHEM	350				
Db	290	FQTKESQETLHK	FASKPASFVKILDTPEKLUFTLQKKIYVIEGTS	KODLTSFNML	349				
Qy	351	SOEGFSAIATNS	GPLLSTVGSYDWAGVVF	-LYTTSKEKSTFINNTRVDSNMNDAYLGVAAA	409				
Db	350	SSSGISADLSR	GHAVGAVGAKWAGGFLDLKADLQD	TFIGNEPLTPVVRAGVLGYTVT	409				
Qy	410	-IILNRNVQSL	VLGAPRYQHIGLVAMFR	-QNTGMWESNANVKGTQITGVFGASLCSVDV	466				
Db	410	WLPSRQKTSLL	ASGAPRYQHMRVLLFQEPQGGHWSQVOTIHGTQ	IGSYFGGELCGVDV	469				
Qy	467	DSNGSDDLVLIG	APHYEQTRGGOVSVCPILPRGORARWQCD	AV--LYGEOGQPNWRGAA	524				
Db	470	QDQGETELLIG	APLFFYGEORGGRVFY	----QRQLGFEEVSELOQDGPYILGRFGEA	524				
Qy	525	LTVLGDVNGDKL	TDVAITGAPGEEDNRGAVYLFHGTSGS	GISPSHRSORIAGSKLSPRLQYF	584				
Db	525	ITALTDINGDL	VDVAVGAPLEE	-QGANVIFNGRHG-GLSPQSPQRIEGTVL	SGLOWP	581			
Qy	585	GQSLSGQDITM	QGLVDLTVGAQGHVLLLSQPVLRYKAIWENF	PREVARNVFECNQVV	644				
Db	582	GRSITHGVKLE	GDGLADVAVGAESQMIIVLSRPVDMVTLM	SFSPABIPVHEVECSYSTS	641				
Qy	645	-KGKEAGEVRV	CLHVQKSTRDLREGQIQSVVTYDLALD	SGRPHSRAVFNETKNSTROT	703				
Db	642	NMKKEGYNIT	ICFOI-KSLYQPF-QGRGLVANLTYTLQ	LDGHRTRRRLGFLPGGRHLEARNI	699				
Qy	704	QVLGLTOTCT	LKLQLPNCIEDPVSPIVLRNFSL	--VGTPLS--AFGN-----LRPVL	753				
Db	700	AVT-TSMSC	TDSPFHPVCVQDLISPLNVSINLSLWEEB	GTPRDQAGKDIPPLRPSL	758				
Qy	754	AEDAQRLLTAL	PFPEKNCGNNDICQDLSITFSFMSLDCL	VWVGREFNVTVTVNRDGED	813				
Db	759	HSETWEI	----PFPEKNGEDKKCEANLRVSFSPARS	RALRLTAFASLSVELSLSNLEED	813				
Qy	814	SYRTQVTFP	PLDLSYRKVSTLQNRQSRWRLACES	--ASSTEVSGALKSTCSINHPI	871				
Db	814	AYWQLDLHP	PPGLSFRKVEML---	KPHSQIPVSCSELPEESRLLSRAL---	SCNVSSPI	867			
Qy	872	FPENSEVT	FNITPDVDKASLGNKLLKANVTSSNN	---MPTNKTKEFQLELPAVKVAVY	927				
Db	868	FKAGHSVALQ	MMFNTLVNSWGDSVELHANVTCNNED	SDLLLEDNSATTI---IPILYPIN	924				
Qy	928	MVVTSHGV	STKYLNFTASENTSRVMQHQYQV	---SNLQGRSLP-ISLVFLVPLVRLNQT	983				
Db	925	ILIQDQED	STLYVSTFKPKPIHQVKMYQVRIQPSI	HDHNIPLEAVGVGPQPSGPI	984				
Qy	984	WDRPQVTF	SENLSSTCHTK--ERLPSHD--FLAELRKA	PVWNCIAVQRIQCIDI	PFPG	1039			
Db	985	THOWSVMQ	EPVP--PCHYEDLERLPDAEPCPLGAL	PCPVPW-----	1024				

Qy	1040	IQBEFNATLKGNSLFDWYIKTSNHHLLIVTAEILFNDSVFTLLPGGAFVRSQTETKVE	1099
Db	1025	FRQBIQLVQVIGTLELNGVEIAS-SMFSLGSLGSLSFNSSSHFLYGSNASL-AQVVMKVD	1082
Qy	1100	PFEVPNPFLPIVGVSSVGLLILLALITAAALVKLGFFKQYKDMKSEG-GPPGAEP	1152
Db	1083	VYVEKQMLYLYVLSGIGGLLLLLLIFIVLYKVGFFRNKLKEMKAGKGVNGIP	1136
RESULT 13			
Q6TVB8	Q6TVB8	PRELIMINARY;	PRT; 1166 AA.
AC	Q6TVB8		
DT	05-JUL-2004	(TrEMBLrel. 27, Created)	
DT	05-JUL-2004	(TrEMBLrel. 27, Last sequence update)	
DT	05-JUL-2004	(TrEMBLrel. 27, Last annotation update)	
DE	Lymphocyte function-associated antigen 1 alpha subunit CD11a.		
OS	Bos taurus (Bovine).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutazoa; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
OC	Bovinae; Bos.		
OX	NCBI_TaxID=9913;		
RP	[1]		
RP	SEQUENCE FROM N.A.		
RA	Dileepan T., Thumbikat P., Kannan M.S., Maheswaran S.K.;		
RL	Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.		
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).		
CC	-1- SIMILARITY: Belongs to the integrin alpha chain family.		
DR	EMBL; AY382558; AAQ90015.1; -		
DR	InterPro; IPR000413; Integrin_alpha.		
DR	InterPro; IPR002035; VWF_A.		
DR	Pfam; PF01839; FG-GAP; 1.		
DR	Pfam; PF00357; Integrin_alpha; 1.		
DR	Pfam; PF00092; VWA; 1.		
DR	PRINTS; PR01185; INTEGRINA.		
DR	PRINTS; PR00453; VWFADOMAIN.		
DR	SMART; SM00191; Int_alpha; 5.		
DR	SMART; SM00327; VWA; 1.		
DR	PROSITE; PS00242; INTEGRIN_ALPHA; 1.		
DR	PROSITE; PS00234; VWFA; 1.		
KW	Cell adhesion; Integrin; Transmembrane.		
SQL	SEQUENCE 1166 AA; 128723 MW; 7B8D8AFBA896C9DF CRC64;		
Query Match 26.2%; Score 1557; DB 2; Length 1166;			
Best Local Similarity 34.2%; Pred. No. 2.5e-93;			
Matches 411; Conservative 203; Mismatches 478; Indels 108; Gaps 34;			
Qy	1	MALRVLLLTALTL--CHGFNLDTENAMTFQENARG--FGSVVQLQSGSVVVGAPQIIVA	56
Db	7	IVRLLSGGFVFAPAWSYNLDVRHVQNFSPFPLAGRHFGVRVLQV-GNGVVVGAPSE---	62
Qy	57	ANORGSILYCDYSTGSCPEIRLOVPVEAVNMSLGLSLAATTPPQLACGPTVHQTCSEN	116
Db	63	GNSMGNLYQCPETGDCPLVTLS--SNYSKYLGMTLATDPTSDNLACDPLGLSRTCDQN	120
Qy	117	TVYKGLCLFGSNLRQOPQFPFALRCCPOEDSDIAFLIDGSGSIIPHDFRMKEFVSTV	176
Db	121	IYLSGLCYLLHENLRGVLGPHGFCYQECIKGNVDLFLFDGMSLQODEFEKIVDFMKDV	180
Qy	177	MEOLKKSKTFLSLMQYSEEPRIHFTKFQNNPNRSLVKRPIQTQLGRTHTATGIRKVR	236
Db	181	MKLSNYSYQFAAVQSFYTFETFDLYIKQKDPDALLAGVKHMLLTNTFGAINYVAK	240
Qy	237	ELFNITNGARKNAFKILVITDGEKGDPLGYEDVITPEADREGVIRVVIQVGDAPREKS	296
Db	241	EVFRPDIGARPDATKVLIIITDGK--PPTNTTLMRPKTS--RSLLGIGKNFKTKES	293
Qy	297	ROELNTIAKPPRDHYFQVNNFEALKTIQNLRKFAISGTQTGSSSFEHEMSQGFPS	356
Db	294	QEAHQFAPQKPSBEFVKILDTFKLIDLFELQKKYIVIEGTSKQDLSFNMELSSSGIS	353
Qy	357	AAITNSGPIILSTVGSYDWAGGVF-LYTSKEKSTFINNTRVDSMDNDAYLVGAAA-IILRN	414

Db 354 ADLSGHHVAVGAKDWAGGLDLKADLKSSTFGNEPLTVESRAGLYGTVTRLPKRG 413
Qy 415 RVQSLVIGAPRYOHTGLVAMFRQ--NTGMWESNANVKGTQICAYGASCLSDVDVDSNGST 472
Db 414 TMSLLATGAPKYQHVRVLLFQPKRGFPWSQIQBIDIGIQISYFGSLCGVDVDRDGET 473
Qy 473 DLVLIGAPHYEOTRGGOVSVCPPLRGORARQCDVAVLYGEOGPWGRFGAALTVLGDVN 532
Db 474 ELLLTAAFLYGEORGRVFIY---QKIQLEFQWVSELOGETGYPLGRFGAIAALTIN 530
Qy 533 GDKLTVAIGAPGEDNRGAVLFGHTSGSISPSHSQRIAGSKLSPRLQVFGSLSGGQ 592
Db 531 GDELTDVAVGAPLEB--QGAVYIFNGQOG--GLSPRPSQRIEQTQMFSGIQWFGSIHGK 587
Qy 593 DLTMGLVDLTVGAQGHVLLRSQPLRVKAIMFNPREVARNVPECNDQVVKKEAG-E 651
Db 588 DLGGDLADVAVGAEQVILSSRPVDDIITSVSFSPAEPVHEVECSYSTSNQKKEGVN 647
Qy 652 VRVCLHVQK--STRDLREGQIQSVVTVDLALDSGRPHSRVAFNETKSTRQTQVLGIT 709
Db 648 LTVCFQVKSLSLT-----FQGHVLANLTYTLQDGHRTSRGLFPGGKHKLIGNTAVTPV- 702
Qy 710 QTCETLKLQPCNIEDPVPSPVLRNLSL---VGTPLS--AFGNLRPVLAEADAQLFTAL 764
Db 703 KSCFVFWFHPFICIQDLISPINVLSYSLSWEDEGTFRDPRALDRDIPPIKPSPHLETKE 762
Qy 765 PFPEKNCNDNICQDDLSITFSFMSLDCLVGGPREFNVTVVRNDGDSVTRQTQVTFPP 824
Db 763 IPFEKNCEDKNCEADKLAFSDMRSKILRLTPSASLSVRLTLRNTABDAYVQVTLSP 822
Qy 825 LDLSYKRVSTLQNRQSQRSLACESASSTVSGALKSTSCSINHPIPPENSEVTFNTF 884
Db 823 QGLSPRKVEIL---KPHSHVPVGCBELPEAVVHS--RALSNCVSSPIFGESMDIOWMF 878
Qy 885 DVDSKASLGNKLLKANVTS-----ENNMPRTNKTEFQLELPVKYAVYVMTSHGVS 936
Db 879 NTLQKSGMDGFELQANVCNNEDSLLLEDNSATTS-----IPVMYPINVLTKDQENS 931
Qy 937 TKYLNFTASNTSRVMQHQYQV---SNLQORSPLISLVFLVPLVRLNQTIV---WD---R 986
Db 932 TLVIGFTPKSPRIHHVKHLYQVRIQPSNYDNMP--FLEALVRVPRVHSEGLITHKWSIQME 990
Qy 987 POWTFS--ENLSSTCHTKERLPSSHDFLAEELKAPVNVCSIAVCORIQCDIPFGIQEBFN 1045
Db 991 PFVNCSPRNLESDEAE-----SCSFGI--BFRCPIDF--RQELT 1027
Qy 1046 ATLKNLSPDWIKTSHNHLIVSTAEILFNDVSVFTLLPQCGAFVRSQTETKVEPPEVFN 1105
Db 1028 VQVNGMVELRGTIKAS--SMLSLSCLSLAISFNSSKHFLHGRNASM--AQVVMKVDLVYEKE 1085
Qy 1106 PLPLTVGSSVGGILLALLALITALYKLGFPKROYKDM-----SEGGPPGAEPO 1153
Db 1086 MLYVYLSGIGLULLLFLIFIALYKVGFPKRNKMEANVDASSEIPGEDAGQPELEKE 1145

RESULT 14

AAQ90015 PRELIMINARY; PRT; 1166 AA.
AC AAQ90015, (Tremblrel. 27, Created)
DT 02-MAR-2004 (Tremblrel. 27, Last sequence update)
DT 02-MAR-2004 (Tremblrel. 27, Last annotation update)
DE Lymphocyte function-associated antigen 1 alpha subunit CD11a.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Dillepan T., Thumikak P., Kannan M.S., Maheswaran S.K.;
RT "Molecular cloning and sequencing of bovine CD11a.";

RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY382558; AAQ90015.1; -.
SQ SEQUENCE 1166 AA; 128723 MW; 7B8D8AFBA896C9DF CRC64;
Query Match 26.2%; Score 1557; DB 2; Length 1166;
Best Local Similarity 34.2%; Pred. No. 2.5e-93;
Matches 411; Conservative 203; Mismatches 478; Indels 108; Gaps 34;
Qy 1 MALVLLVLLTALT--CHGFNLDTENAMTFQENARG--FGQSVVOLQSGRVVVGPOEIVA 56
Db 7 IVLRLLSGPPVAFAPANSYNDVRHVQVSPPLAGRHFGYVLQV--GNGVVVGAPSE--- 62
Qy 57 ANORGSLYQCDYSTGCEPIRLQVPVEAVNMNLSGLSAAATSPQLLACGPTVHTQTCSEN 116
Db 63 GNSMGNLYQCQPETGDCPLVTL--SNYTSKYLGWTLATDPTSDNLLACDPLGSRCTQDN 120
Qy 117 TVYKGLCHLFGSNLRQOPKQPEALRGCPQSDSDIAFLIDGSGSIIIPDPRMKEFVSTV 176
Db 121 IYLSGLCYLIHENLRGPVLQGHGPGYQECIKGNVDLVFLFDGMSLQDQDEFKIVDFMKDV 180
Qy 177 MEOLKSKTFLSLMOYSEBPIHFTFEFQNNPNRSLVKPITOLLGRTHTATGIRKVV 236
Db 181 MKLNSNSYQFAAQVSTYFTEFTFLDYIKQDPDALLAGVKHMLLTNTFGAINYAK 240
Qy 237 ELFNITGARKNAFKILVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVDAPRSK 296
Db 241 EVFRPDLGARPDATKVLIIITDGK---PPTNTLMRPKTS---RSLGIGKFKTKES 293
Qy 297 ROELNTASKPRPHVFOVNNFEALKITQNLREKXFAIEGTQTCGSSSPEHMSQEGFS 356
Db 294 QEALHQFASKVEFVFKILDTFEKLKDLFTLQKIVYIEGTSKODLTSFNMSLSSSGIS 353
Qy 357 AAITNSGPLLSTGSDYDWAGVF--LYTSKESKTFINMTVRVSDMNDAYLVGAAA--IILRN 414
Db 354 ADLSEGHVGVAGAKDWAGGLDLKADLKSSTFGNEPLTVESRAGLYGTVTRLPKRG 413
Qy 415 RVQSLVIGAPRYOHTGLVAMFRQ--NTGMWESNANVKGTQICAYGASCLSDVDVDSNGST 472
Db 414 TMSLLATGAPKYQHVRVLLFQPKRGFPWSQIQBIDIGIQISYFGSLCGVDVDRDGET 473
Qy 473 DLVLIGAPHYEOTRGGOVSVCPPLRGORARQCDVAVLYGEOGPWGRFGAALTVLGDVN 532
Db 474 ELLLTAAFLYGEORGRVFIY---QKIQLEFQWVSELOGETGYPLGRFGAIAALTIN 530
Qy 533 GDKLTVAIGAPGEDNRGAVLFGHTSGSISPSHSQRIAGSKLSPRLQVFGSLSGGQ 592
Db 531 GDELTDVAVGAPLEB--QGAVYIFNGQOG--GLSPRPSQRIEQTQMFSGIQWFGSIHGK 587
Qy 593 DLTMGLVDLTVGAQGHVLLRSQPLRVKAIMFNPREVARNVPECNDQVVKKEAG-E 651
Db 588 DLGGDLADVAVGAEQVILSSRPVDDIITSVSFSPAEPVHEVECSYSTSNQKKEGVN 647
Qy 652 VRVCLHVQK--STRDLREGQIQSVVTVDLALDSGRPHSRVAFNETKSTRQTQVLGIT 709
Db 648 LTVCFQVKSLSLT-----FQGHVLANLTYTLQDGHRTSRGLFPGGKHKLIGNTAVTPV- 702
Qy 710 QTCETLKLQPCNIEDPVPSPVLRNLSL---VGTPLS--AFGNLRPVLAEADAQLFTAL 764
Db 703 KSCFVFWFHPFICIQDLISPINVLSYSLSWEDEGTFRDPRALDRDIPPIKPSPHLETKE 762
Qy 765 PFPEKNCNDNICQDDLSITFSFMSLDCLVGGPREFNVTVVRNDGDSVTRQTQVTFPP 824
Db 763 IPFEKNCEDKNCEADKLAFSDMRSKILRLTPSASLSVRLTLRNTABDAYVQVTLSP 822
Qy 825 LDLSYKRVSTLQNRQSQRSLACESASSTVSGALKSTSCSINHPIPPENSEVTFNTF 884
Db 823 QGLSPRKVEIL---KPHSHVPVGCBELPEAVVHS--RALSNCVSSPIFGESMDIOWMF 878
Qy 885 DVDSKASLGNKLLKANVTS-----ENNMPRTNKTEFQLELPVKYAVYVMTSHGVS 936
Db 879 NTLQKSGMDGFELQANVCNNEDSLLLEDNSATTS-----IPVMYPINVLTKDQENS 931
Qy 937 TKYLNFTASNTSRVMQHQYQV---SNLQORSPLISLVFLVPLVRLNQTIV---WD---R 986

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2005, 14:59:41 ; Search time 215.571 Seconds
(without alignments)
1918.696 Million cell updates/sec

Title: RWULB-A

Perfect score: 5953

Sequence: 1 MALRVLLTALTLCGFNLD.....FKRQYKMMSEGGPGABPQ 1153

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5953	100.0	1153	2	AAW65090 Human Bet
2	5953	100.0	1153	3	AAW65090 Human CD1
3	5953	100.0	1153	5	AAU80252 Human Int
4	5953	100.0	1153	5	ABG61469 Human Bet
5	5953	100.0	1153	5	AAO14428 Integrin
6	5953	100.0	1153	7	ADP25615 Binding d
7	5943	99.8	1153	2	AAW65091 Human sub
8	5937.5	99.7	1152	8	ADM99589 Human Int
9	5930.5	99.6	1152	8	ADP12435 Protein e
10	3514	59.0	1163	8	ADP44061 Human CD1
11	3500	58.8	1163	8	ADN02004 Human inf
12	3500	58.8	1163	8	ADQ17510 Human sof
13	3491	58.6	1163	2	AAW65091 Human bet
14	3477	58.4	1163	3	AAW65091 Human Bet
15	3477	58.4	1163	3	AAW65091 Human CD1
16	3477	58.4	1163	6	ABG61470 Human Bet
17	3475	58.4	1163	6	ABU07406 Protein d
18	3475	58.4	1163	7	ADG32005 Human hom
19	3452	58.0	1161	2	AAW78166 Human bet
20	3452	58.0	1161	2	AAW23049 Human bet
21	3452	58.0	1161	2	AAW57491 Human bet
22	3452	58.0	1161	2	AAW65089 Human Bet
23	3452	58.0	1161	2	AAW72825 Human alp
24	3452	58.0	1161	2	AAW73342 Human alp
25	3452	58.0	1161	3	AAW67359 Human alp

RESULT 1
AAW65090
ID AAW65090 standard; protein; 1153 AA.

XX AC AAW65090;

XX DT 28-SEP-1998 (first entry)

XX DE Human Beta-integrin CD11b subunit protein.

XX KW Beta-integrin alpha-d subunit; human; modulator; treatment; psoriasis;

XX KW type-1 diabetes; atherosclerosis; multiple sclerosis; asthma;

XX KW lung inflammation; acute respiratory distress syndrome; CD11b subunit;

XX KW rheumatoid arthritis.

XX OS Homo sapiens.

XX PN US5728533-A.

XX PD 17-MAR-1998.

XX PF 07-JUN-1995; 95US-00485618.

XX PR 23-DEC-1993; 93US-00173497.

XX PR 05-AUG-1994; 94US-00286889.

XX PR 21-DEC-1994; 94US-00362652.

XX PA (ICOS-) ICOS CORP.

XX PI Van Der Vieren M, Gallatin WM;

XX WPI; 1998-206565/18.

XX Screening assay for modulators of integrin binding - using immobilised or

XX labelled alpha-d polypeptide, useful for, e.g. treating type-I diabetes.

XX Example 5; Fig 1A-D; 106pp; English.

This sequence represents a human beta-integrin CD11b subunit which is used to describe a method for identifying compounds that modulate the interaction of the beta-integrin alpha-d subunit with a binding partner of alpha-d which involves contacting an alpha-d polypeptide with an alpha-d binding partner, one of which is immobilised and the other of which is labelled, in the presence of a test compound, and determining if the compound affects binding between the alpha-d polypeptide and alpha-d binding partner, where the alpha-d polypeptide is alpha-d or its fragment comprising the cytoplasmic, transmembrane or extracellular domain of alpha-d. Compounds that modulate alpha-d binding could be used to treat

CC diseases such as type-I diabetes, atherosclerosis, multiple sclerosis,
CC asthma, psoriasis, lung inflammation, acute respiratory distress syndrome
CC and rheumatoid arthritis
XX
SQ Sequence 1153 AA;

Query Match 100.0%; Score 5953; DB 2; Length 1153;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	MALRVLLTALTLCHGNLDTENAMTFQENARGFGQSVVLOGSRVVVGAPEIIVAAQR	60
DB	1	MALRVLLTALTLCHGNLDTENAMTFQENARGFGQSVVLOGSRVVVGAPEIIVAAQR	60
QY	61	GSLYQCDYSTGCEPIRLQVPVEAVNMSLGLSLAATTGPPOLLACGPTVHOTCSSENTYVK	120
DB	61	GSLYQCDYSTGCEPIRLQVPVEAVNMSLGLSLAATTGPPOLLACGPTVHOTCSSENTYVK	120
QY	121	GLCFIFGNLRQOPKQPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQL	180
DB	121	GLCFIFGNLRQOPKQPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQL	180
QY	181	KSKTFLPSLMQVSEEFRIHFTKFEQNNPNRSLVKPITOLLGRTHATGIRKVVRELFN	240
DB	181	KSKTFLPSLMQVSEEFRIHFTKFEQNNPNRSLVKPITOLLGRTHATGIRKVVRELFN	240
QY	241	ITNGARKNAFKILVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVDGDAFRSEKSRQEL	300
DB	241	ITNGARKNAFKILVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVDGDAFRSEKSRQEL	300
QY	301	NTIASKPRDRHVQVNNPEALKTIQNLREKPAIEGTQTSSSSFEHEMGOEFSAAIT	360
DB	301	NTIASKPRDRHVQVNNPEALKTIQNLREKPAIEGTQTSSSSFEHEMGOEFSAAIT	360
QY	361	SNGPLLSTVGSVDMAGGVFLYTSKEKSTFINNTRVDSMDNDAYLGYAAIILNRVQSLV	420
DB	361	SNGPLLSTVGSVDMAGGVFLYTSKEKSTFINNTRVDSMDNDAYLGYAAIILNRVQSLV	420
QY	421	LGAPRYQHIGLVAMFRQNTGMWESNANVKGITQIGAYFGASLCSVDVDSNGSTDVLIGAP	480
DB	421	LGAPRYQHIGLVAMFRQNTGMWESNANVKGITQIGAYFGASLCSVDVDSNGSTDVLIGAP	480
QY	481	HYEOTRGQGVSVCPPLRGORARWOCDAVLIGEQQPWGRFGAALTIVLDVNGDKLTJVA	540
DB	481	HYEOTRGQGVSVCPPLRGORARWOCDAVLIGEQQPWGRFGAALTIVLDVNGDKLTJVA	540
QY	541	IGAPGEEDNRGAVYLFHGTSGSISPSHSORITAGSKLSPRLQYFGQSLSGGQDLTMDGLV	600
DB	541	IGAPGEEDNRGAVYLFHGTSGSISPSHSORITAGSKLSPRLQYFGQSLSGGQDLTMDGLV	600
QY	601	DLTVGAQGHVLLRSQPVLRVKAIMEFNPREVARNVFECDNQVVKGEAGEVRVCLHVQK	660
DB	601	DLTVGAQGHVLLRSQPVLRVKAIMEFNPREVARNVFECDNQVVKGEAGEVRVCLHVQK	660
QY	661	STRDLREGQIQSVVTVYDLDLSDGRPHRAVNETKNSRTRQTVLGLTQTCETLKUQLP	720
DB	661	STRDLREGQIQSVVTVYDLDLSDGRPHRAVNETKNSRTRQTVLGLTQTCETLKUQLP	720
QY	721	NCIEDPVSPVLRNLSVGTPLSAFGLNRPVLAEADAORLFTALPPFEKNGCNDNICODD	780
DB	721	NCIEDPVSPVLRNLSVGTPLSAFGLNRPVLAEADAORLFTALPPFEKNGCNDNICODD	780
QY	781	LSITFSFMSLDCVLVGGPREFNTVTVRNDGEDSVRTQVTFPPDLDSYRKVSTLQNRQ	840
DB	781	LSITFSFMSLDCVLVGGPREFNTVTVRNDGEDSVRTQVTFPPDLDSYRKVSTLQNRQ	840
QY	841	QSRNLACESASSTEVSGALKSTSCINHPFEPENSEVTFNITFDVDSKASLGNKLLKA	900
DB	841	QSRNLACESASSTEVSGALKSTSCINHPFEPENSEVTFNITFDVDSKASLGNKLLKA	900
QY	901	NVTSENNNPRNTKTEFQLELPKVAVMVMTSHGVSTKYLNFTASNTSRVWQHOYQVSN	960
DB	901	NVTSENNNPRNTKTEFQLELPKVAVMVMTSHGVSTKYLNFTASNTSRVWQHOYQVSN	960

QY	961	LGQSLPISLVFLVPVRLNQTWIDRPOVTFSENLSSTCHTKERLPSSHSDFLAELRKAPV	1020
DB	961	LGQSLPISLVFLVPVRLNQTWIDRPOVTFSENLSSTCHTKERLPSSHSDFLAELRKAPV	1020
QY	1021	VNCSTAVCORIQCDIPFFGIQEEFNATLKGNLSPDWYIKTSHNHLILVSTABILFNDVSF	1080
DB	1021	VNCSTAVCORIQCDIPFFGIQEEFNATLKGNLSPDWYIKTSHNHLILVSTABILFNDVSF	1080
QY	1081	TLLPCQGAFAVSQETKVEPEVNPPLPLIYGVSSVGGLLILALITAAALYKLGFFKRYKD	1140
DB	1081	TLLPCQGAFAVSQETKVEPEVNPPLPLIYGVSSVGGLLILALITAAALYKLGFFKRYKD	1140
QY	1141	MWSEGGPPGAEPQ 1153	
DB	1141	MWSEGGPPGAEPQ 1153	
RESULT 2			
AAB07360			
ID	AAB07360	standard; protein; 1153 AA.	
XX	AAB07360;		
AC	AAB07360;		
XX			
DT	17-JAN-2001	(first entry)	
XX			
DE	Human CD11b	protein sequence.	
XX			
KW	Human; macrophage infiltration inhibition; alpha_d integrin;		
KW	leukocyte integrin; Leu-CAM; leukointegrin; immune response;		
KW	inflammation; leukocyte adhesion deficiency; LAD; Type I diabetes;		
KW	atherosclerosis; multiple sclerosis; asthma; psoriasis; beta2 integrin;		
KW	lung inflammation; acute respiratory distress syndrome; Crohn's disease;		
KW	rheumatoid arthritis; central nervous system injury; CD11b.		
XX			
OS	Homo sapiens.		
XX			
FN	WO200029446-A1.		
XX			
PD	25-MAY-2000.		
XX			
PF	16-NOV-1999;	99WO-US027139.	
XX			
PR	16-NOV-1998;	98US-00193043.	
PR	08-JUL-1999;	99US-00350259.	
XX			
PA	(ICOS-) ICOS CORP.		
XX			
PI	Gallatin MW, Van Der Vieren M;		
XX			
DR	WPI; 2000-387751/33.		
PT			
PT	Use of novel anti-alpha integrin d monoclonal antibodies to inhibit		
PT	macrophage infiltration and reduce inflammation at central nervous system		
XX			
PS	injury sites.		
XX			
XX	Example 5; Fig 1; 270pp; English.		
CC			
CC	Integrins are a class of membrane-associated molecules that participate		
CC	in cellular adhesion. Integrins are made up of an alpha subunit and a		
CC	beta subunit. One class of human integrins are restricted to expression		
CC	in white blood cells and have a common beta2 subunit: the leukocyte		
CC	integrins, Leu-CAMs, leukointegrins or beta2 integrins. Beta2 integrins		
CC	have an important role in immune and inflammatory responses. The present		
CC	protein sequence is the human integrin alpha subunit CD11b. This sequence		
CC	was used in an alignment to identify a novel beta2 integrin alpha		
CC	subunit: alpha_d (AAA60014 and AAB07359). The present sequence has		
CC	approximately 60% identity to the protein sequence of alpha_d. The		
CC	Alpha_d gene and protein may be useful in therapy for diseases linked to		
CC	aberrant alpha_d function e.g. Type I diabetes, atherosclerosis, multiple		
CC	sclerosis, asthma, psoriasis, lung inflammation, acute respiratory		
CC	distress syndrome, rheumatoid arthritis and leukocyte adhesion deficiency		
CC	(LAD). In addition, anti-alpha_d monoclonal antibodies may be used in the		

CC inhibition of macrophage infiltration at the site of a central nervous
CC system injury. The monoclonal antibodies can also be used to detect and
CC diagnose Crohn's disease
XX
SQ Sequence 1153 AA;

Query Match 100.0%; Score 5953; DB 3; Length 1153;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALRVLTLTALTLCHGFLNDTENAMTFQENARGFQGVVQLQSGSRVVVGAPEIIVAAQR 60
DB 1 MALRVLTLTALTLCHGFLNDTENAMTFQENARGFQGVVQLQSGSRVVVGAPEIIVAAQR 60
QY 61 GSLYQCDYSTGCEPIRLQVPVEAVNMSLGLSLAATTSPQALLACGPTVHOTCSENTYVK 120
DB 61 GSLYQCDYSTGCEPIRLQVPVEAVNMSLGLSLAATTSPQALLACGPTVHOTCSENTYVK 120
QY 121 GLCFLFGNLRQOPKFPPEARLRCQEDSDIAFLIDGSGSIIPHDFRMKSFVSTVMEQL 180
DB 121 GLCFLFGNLRQOPKFPPEARLRCQEDSDIAFLIDGSGSIIPHDFRMKSFVSTVMEQL 180
QY 181 KSKTFLFSLMOYSEEFRIHFTFKFQNNPNRSLVKPITQLLGRTHATGIRKVVRELPN 240
DB 181 KSKTFLFSLMOYSEEFRIHFTFKFQNNPNRSLVKPITQLLGRTHATGIRKVVRELPN 240
QY 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQEL 300
DB 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQEL 300
QY 301 NTIASKPRDRHVQVNNPEALKTIONQREKFAJEGTQTGSSSSFEHEMSQEGFSAAIT 360
DB 301 NTIASKPRDRHVQVNNPEALKTIONQREKFAJEGTQTGSSSSFEHEMSQEGFSAAIT 360
QY 361 SNGPLSTVGSYDMAGGVPLTYSKEKSTFINNTRVDSMDNDAYLGYAAIILRNREVSLV 420
DB 361 SNGPLSTVGSYDMAGGVPLTYSKEKSTFINNTRVDSMDNDAYLGYAAIILRNREVSLV 420
QY 421 LGAPRYQHIGLVAMPFRONTGMWESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLIGAP 480
DB 421 LGAPRYQHIGLVAMPFRONTGMWESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLIGAP 480
QY 481 HYEOTRGQGVSVCPPLRGQARWOCDAVLGEGQCPWGRFGAALTIVLDVNGDKLTDVA 540
DB 481 HYEOTRGQGVSVCPPLRGQARWOCDAVLGEGQCPWGRFGAALTIVLDVNGDKLTDVA 540
QY 541 IGAPGEENRGAVALPHGTSGSIGSPHSQRTAGSKLSPRLQYFGQSLGGQDLTMDGLV 600
DB 541 IGAPGEENRGAVALPHGTSGSIGSPHSQRTAGSKLSPRLQYFGQSLGGQDLTMDGLV 600
QY 601 DLTGVAQGHVLLRSQPVLRVKAINFEFNPREVARNVFECDQVVKGEAGEVRVCLHVQK 660
DB 601 DLTGVAQGHVLLRSQPVLRVKAINFEFNPREVARNVFECDQVVKGEAGEVRVCLHVQK 660
QY 661 STRDLREGQIQSVVTVYDLALDSGRPHSAVNETKNSTRQTQVLGTQTCTETLKQLP 720
DB 661 STRDLREGQIQSVVTVYDLALDSGRPHSAVNETKNSTRQTQVLGTQTCTETLKQLP 720
QY 721 NCIEDPVSPVLRNLFSLVGTPLSFAFNLRPLVLAEDAQRLLFTALPPEKNCNDNICODD 780
DB 721 NCIEDPVSPVLRNLFSLVGTPLSFAFNLRPLVLAEDAQRLLFTALPPEKNCNDNICODD 780
QY 781 LSITPSFMSLDCLVVGGPREFNVTVVRNDGSDSYRTQVTFPPDLDSYRKVSTLQNR 840
DB 781 LSITPSFMSLDCLVVGGPREFNVTVVRNDGSDSYRTQVTFPPDLDSYRKVSTLQNR 840
QY 841 QRSWLACESASSTVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLKA 900
DB 841 QRSWLACESASSTVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLKA 900
QY 901 NVTSENMPRTNKTFFOLELPVKYAVVMVTVSHGVSTKYLNFTASENTRVMQHOYQVSN 960
DB 901 NVTSENMPRTNKTFFOLELPVKYAVVMVTVSHGVSTKYLNFTASENTRVMQHOYQVSN 960

QY 961 LGQSLPISLVFLVPLVRLNQTVIWDPRQVTFSENLSSTCHTKERLPSSHDFLAELRKAPV 1020
DB 961 LGQSLPISLVFLVPLVRLNQTVIWDPRQVTFSENLSSTCHTKERLPSSHDFLAELRKAPV 1020
QY 1021 VNCISAVCORIQCDIPPFQIOEEFNATLKGNSFDWYIKTSHNHLIIYSTAEILFNDVSF 1080
DB 1021 VNCISAVCORIQCDIPPFQIOEEFNATLKGNSFDWYIKTSHNHLIIYSTAEILFNDVSF 1080
QY 1081 TLLPQOGAFVRSQETKVEPEVPNPLPLIYGVSSVGGLLALLALITAAALYKLGFFRQYKD 1140
DB 1081 TLLPQOGAFVRSQETKVEPEVPNPLPLIYGVSSVGGLLALLALITAAALYKLGFFRQYKD 1140
QY 1141 MWSEGGPPGAEPPQ 1153
DB 1141 MWSEGGPPGAEPPQ 1153

RESULT 3
AAU80252
ID AAU80252 standard; protein; 1153 AA.
XX AC AAU80252;
XX DT 15-JUL-2002 (first entry)
XX Human integrin 1 alpha-M subunit protein.
XX DE Integrin; antiinflammatory; immunosuppression; nephritis; dermatitis;
XX KW inflammatory disease; autoimmune disorder; Crohn's disease;
XX KW human immunodeficiency virus; HIV; myocardial infarction;
XX KW Sjorgen's syndrome; rheumatoid arthritis.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Misc-difference 499..500 /note= "Encoded by GCG CAG AGG"
FT WO200218583-A2.
XX PN 07-MAR-2002.
XX PD 31-AUG-2001; 2001WO-US027227.
XX PF 01-SEP-2000; 2000US-0229700P.
XX PR (BLOO-) CENT BLOOD RES INC.
XX PA Springer TA, Shimoaka M, Lu C;
XX PI WPI; 2002-382964/41.
XX DR N-PSDB; ASK50046.
XX Modified integrin-I or integrin I-like domain polypeptide useful as an immunogen to produce antibodies specific to polypeptide, comprises a disulfide bond such that polypeptide is stabilized in a desired conformation.
XX PS Disclosure; Page 109-112; 112pp; English.
XX This invention relates to a modified integrin-I or integrin I-like domain polypeptide comprising at least one disulfide bond so that the domain is stabilised in a desired conformation. The polypeptide of the invention may have antiinflammatory or immunosuppressive activities. The polypeptides of the invention have an open conformation and are useful as immunogens to produce antibodies that selectively bind to integrin I-domain; and for identifying a modulator of integrin activity, or of interaction of an integrin and a cognate ligand. The polypeptide of the invention, or antibodies (preferably anti-LFA-1 antibody) is useful for treating or preventing an integrin mediated disorder which is an inflammatory or autoimmune disorder in a subject and for inhibiting the binding of an integrin to a cognate ligand such as Crohn's disease,

CC nephritis; human immunodeficiency virus (HIV), myocardial infarction,
 CC Sjorgen's syndrome, rheumatoid arthritis, dermatitis. A therapeutic
 CC composition comprising the peptide of the invention is useful for
 CC treating an integrin mediated disorder in a subject. The polypeptides
 CC and/or active or antigenic fragments are useful as reagents for diagnosis
 CC of integrin-mediated disorders. The present sequence represents the human
 CC integrin-1 alpha-M protein subunit used to generate the mutant
 CC polypeptides of the invention
 XX
 SQ Sequence 1153 AA;

Query Match 100.0%; Score 5953; DB 5; Length 1153;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALRVLLTALTLCHEGNDLTENAMTFQENARGQGVVLOGSRVVGAPQEIIVANQR 60
 DB 1 MALRVLLTALTLCHEGNDLTENAMTFQENARGQGVVLOGSRVVGAPQEIIVANQR 60
 QY 61 GSLYQCDYSTGCEPIRLQVPVEAVNMSLGLSLAATTSPPOLLACGPTVHQTCSNTYVK 120
 DB 61 GSLYQCDYSTGCEPIRLQVPVEAVNMSLGLSLAATTSPPOLLACGPTVHQTCSNTYVK 120
 QY 121 GLCFLEGNLRQOPKPFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRMKGFVSTVMEQL 180
 DB 121 GLCFLEGNLRQOPKPFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRMKGFVSTVMEQL 180
 QY 181 KSKTFLSLMOYSEERFTHFTKBPQNNPNSLVKPIITOLLGRTHATGIRKVVRELFN 240
 DB 181 KSKTFLSLMOYSEERFTHFTKBPQNNPNSLVKPIITOLLGRTHATGIRKVVRELFN 240
 QY 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVPEADREGVIRYVIGVDGDAFRSEKSRQEL 300
 DB 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVPEADREGVIRYVIGVDGDAFRSEKSRQEL 300
 QY 301 NTIASKPRDRHVQNNFEALKTQNLQREKXFAIEGTQTGSSSSFEHMGQEGFSAIT 360
 DB 301 NTIASKPRDRHVQNNFEALKTQNLQREKXFAIEGTQTGSSSSFEHMGQEGFSAIT 360
 QY 361 SNGPLLSVGVSDWAGGVFLYTSKEKSTFINWTRVDSMDNDAVLGYAAIILNRNVQSLV 420
 DB 361 SNGPLLSVGVSDWAGGVFLYTSKEKSTFINWTRVDSMDNDAVLGYAAIILNRNVQSLV 420
 QY 421 LGAPRYQHIGLVAMFRONTGMWESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLIGAP 480
 DB 421 LGAPRYQHIGLVAMFRONTGMWESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLIGAP 480
 QY 481 HYYEQTREGGVSVCPPLRGQARWQCDVLYGEOGQPMGRFGAALTVLGDVNGDKLTDVA 540
 DB 481 HYYEQTREGGVSVCPPLRGQARWQCDVLYGEOGQPMGRFGAALTVLGDVNGDKLTDVA 540
 QY 541 IGAPGEDNRGAVYLFHGTSGSGLSPSHSQRIAGSKLSPRLQYFGQSLGGQDLTMDGLV 600
 DB 541 IGAPGEDNRGAVYLFHGTSGSGLSPSHSQRIAGSKLSPRLQYFGQSLGGQDLTMDGLV 600
 QY 601 DLTVGAQGHVLLRSQPVLRVKAIMEFNPREVARNVFECNDQVVKREAGEVRVCLHVQK 660
 DB 601 DLTVGAQGHVLLRSQPVLRVKAIMEFNPREVARNVFECNDQVVKREAGEVRVCLHVQK 660
 QY 661 STRDLREGQIOSVVTYDLDLSDGRPHSRVAFNETKSTRQTOVLGLTQTCETLKLQLP 720
 DB 661 STRDLREGQIOSVVTYDLDLSDGRPHSRVAFNETKSTRQTOVLGLTQTCETLKLQLP 720
 QY 721 NCIEDPVSPIVLRNLFNSVGTPLSAFNLRLPVLAEADQRLFTALFPPEKNGCNDNIQDD 780
 DB 721 NCIEDPVSPIVLRNLFNSVGTPLSAFNLRLPVLAEADQRLFTALFPPEKNGCNDNIQDD 780
 QY 781 LSITFSFMSLDCLVVGPREPNNVTVRNDEGDSYRTQVTFPFLDLSYRKVSTLQNRS 840
 DB 781 LSITFSFMSLDCLVVGPREPNNVTVRNDEGDSYRTQVTFPFLDLSYRKVSTLQNRS 840
 QY 841 QRSWLACESASSTEVSGALKSTSCSINHPIFPENSEVTENITFDVDSKASIGNKLLKA 900

DB 841 QRSWLACESASSTEVSGALKSTSCSINHPIFPENSEVTENITFDVDSKASIGNKLLKA 900
 QY 901 NVTSENMMPRNKTKEFQLELPVKYAVVMVVTSHGVSTKYLNFTASENSTRVMQHQYQVSN 960
 DB 901 NVTSENMMPRNKTKEFQLELPVKYAVVMVVTSHGVSTKYLNFTASENSTRVMQHQYQVSN 960
 QY 961 LGQRSPLTSLVLPVRLNQTVIWDPRQVTFSENLSSCTCHTKERLPSHSDFLAELRKAPV 1020
 DB 961 LGQRSPLTSLVLPVRLNQTVIWDPRQVTFSENLSSCTCHTKERLPSHSDFLAELRKAPV 1020
 QY 1021 VNCISAVCQRIQCDIPFFGIQEEFNATLKGNSLDFWIKTSHNHLIIIVSTAIEILFNDVSF 1080
 DB 1021 VNCISAVCQRIQCDIPFFGIQEEFNATLKGNSLDFWIKTSHNHLIIIVSTAIEILFNDVSF 1080
 QY 1081 TLLPGQAGAFVRSQVETKVEPPEPNPLIIVGSSVGGLLIILALITAAALYKLGFFKRYKD 1140
 DB 1081 TLLPGQAGAFVRSQVETKVEPPEPNPLIIVGSSVGGLLIILALITAAALYKLGFFKRYKD 1140
 QY 1141 MMSEGGPPGAEPPQ 1153
 DB 1141 MMSEGGPPGAEPPQ 1153

RESULT 4
 ABG61469
 ID ABG61469 standard; protein; 1153 AA.
 XX
 AC ABG61469;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE Human Beta2 integrin alphaCD11b subunit.
 XX
 KW Beta2 integrin; alphaD subunit; CD11c subunit; CD11b subunit; LAD;
 KW leukocyte adhesion deficiency; inflammatory response; diabetes;
 KW multiple sclerosis; arthritis; graft atherosclerosis; neuroprotective;
 KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KW immune complex alveolitis; leukaemia; ICAM-R; VCAM-1; anti-inflammatory;
 KW intracellular cell adhesion molecule; vascular cell adhesion molecule;
 KW locomotor recovery; locomotor damage; locomotor impairment;
 KW autonomic dysfunction; sensory dysfunction; spinal cord injury.
 XX
 OS Homo sapiens.
 XX
 FN WO200230980-A2.
 XX
 PD 18-APR-2002.
 XX
 PF 15-OCT-2001; 2001WO-US032059.
 XX
 PR 13-OCT-2000; 2000US-00688307.
 XX
 PA (ICOS-) ICOS CORP.
 XX
 PI Gallatin WM, Van Der Vieren M;
 XX
 DR WPI; 2002-463260/49.
 XX
 PT Use of an anti-alpha-d monoclonal antibodies for promoting locomotor
 FT recovery, inhibiting locomotor damage, limiting locomotor impairment, or
 FT limiting autonomic and sensory dysfunction following spinal cord injury.
 XX
 PS Example 5; Page 191-194; 270pp; English.
 XX
 CC The invention relates to promoting locomotor recovery, inhibiting
 CC locomotor damage, limiting locomotor impairment, or limiting autonomic
 CC and sensory dysfunction following spinal cord injury by administering an
 CC anti-alpha-d (Beta2 integrin alpha2 subunit) monoclonal antibody to a
 CC spinal cord injury victim. The method also involves the use of a ligand
 CC selected from ICAM-R or VCAM-1 (intracellular cell adhesion molecule,
 CC vascular cell adhesion molecule). The method is useful for promoting
 CC locomotor recovery, inhibiting locomotor damage, limiting locomotor
 CC impairment, or limiting autonomic and sensory dysfunction following

spinal cord injury. In particular, the spinal cord injury comprises compression of the spinal cord. The antibodies are also useful for reducing inflammation at the site of a central nervous system injury. The specification also details the identification of Beta2 integrin alpha d cDNAs and proteins, for use in raising the antibodies. Beta2 integrins are implicated in diseases such as LAD (leukocyte adhesion deficiency, inflammatory response, diabetes, multiple sclerosis, arthritis, graft, atherosclerosis, inflammatory bowel disease, Crohn's disease, ulcerative colitis, immune complex alveolitis and leukaemia. The present sequence is a Beta2 integrin alpha subunit sequence included for comparison with the Beta2 integrin alpha protein sequences

Sequence 1153 AA;

Query Match 100.0%; Score 5953; DB 5; Length 1153;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALRVLLLTALTLCGHNLDTENAMTFQENARGQSVVQLQGRVVVGAPOEIVANQR 60
DB 1 MALRVLLLTALTLCGHNLDTENAMTFQENARGQSVVQLQGRVVVGAPOEIVANQR 60
QY 61 GSLYQCDYSTGCEPIRLQVPVEAVNMSLGLSLAATTSPPOLLACGPTVHOTCSENTYVK 120
DB 61 GSLYQCDYSTGCEPIRLQVPVEAVNMSLGLSLAATTSPPOLLACGPTVHOTCSENTYVK 120
QY 121 GLCFLFGNLRQOQKPEALRGCPQEDSDIAFLIDGSGSIIPHDRMKCFVSTVMEQL 180
DB 121 GLCFLFGNLRQOQKPEALRGCPQEDSDIAFLIDGSGSIIPHDRMKCFVSTVMEQL 180
QY 181 KKSNTLSLMQYSEFRTHFTFKFQNNPNRSLVKPTITQLGRTHATGIRKVVRELFN 240
DB 181 KKSNTLSLMQYSEFRTHFTFKFQNNPNRSLVKPTITQLGRTHATGIRKVVRELFN 240
QY 241 ITGARKNAFKILVITDGEKFGDPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQEL 300
DB 241 ITGARKNAFKILVITDGEKFGDPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQEL 300
QY 301 NTIASKPRDRHVQNNPEALKTIONLREKXFAIEGTQTGSSSSFEHMQEGFSAIT 360
DB 301 NTIASKPRDRHVQNNPEALKTIONLREKXFAIEGTQTGSSSSFEHMQEGFSAIT 360
QY 361 SNGPLSTVGSYDRAGGVFLTSKEKSTFINMTRVDSMDNDAYLGAAIILRRNVQSLV 420
DB 361 SNGPLSTVGSYDRAGGVFLTSKEKSTFINMTRVDSMDNDAYLGAAIILRRNVQSLV 420
QY 421 LGAPRYQHIGLVAMPFRONTGWESNANVKGTOIGAYFCASLCSVDVDSNGSTDVLIGAP 480
DB 421 LGAPRYQHIGLVAMPFRONTGWESNANVKGTOIGAYFCASLCSVDVDSNGSTDVLIGAP 480
QY 481 HYYEQTRGGQVSVCPPLRGQRARWQCDVLYGEOQPMGRFGAALTVLGDVNGDKLTDVA 540
DB 481 HYYEQTRGGQVSVCPPLRGQRARWQCDVLYGEOQPMGRFGAALTVLGDVNGDKLTDVA 540
QY 541 IGARPEEDNRGAVLPHGTSGSGISPSHSORIASKLSPLRYFGQSLSGGQDLTMDGLV 600
DB 541 IGARPEEDNRGAVLPHGTSGSGISPSHSORIASKLSPLRYFGQSLSGGQDLTMDGLV 600
QY 601 DLTGAQGHVLLRSQPVLRVKAIMEFNPREVARNVPECNDQVVKGEAGVRVCLHVQK 660
DB 601 DLTGAQGHVLLRSQPVLRVKAIMEFNPREVARNVPECNDQVVKGEAGVRVCLHVQK 660
QY 661 STRDLREGQIQSVVTVYDLDALDGRPHSRAVFNETKNSRRQTQVGLTQTCETLKLQLP 720
DB 661 STRDLREGQIQSVVTVYDLDALDGRPHSRAVFNETKNSRRQTQVGLTQTCETLKLQLP 720
QY 721 NCIEDPVSPIVRLNFSVLGTPLSAFLGNLRPVLAEADAORLFTALPPFKNGCNDNICODD 780
DB 721 NCIEDPVSPIVRLNFSVLGTPLSAFLGNLRPVLAEADAORLFTALPPFKNGCNDNICODD 780
QY 781 LSITTFSMSLDCLVVGGRPREFNVTVVRNDGEDSVRTQVTFEPLDLSYRKVSTLQNGRS 840
DB 781 LSITTFSMSLDCLVVGGRPREFNVTVVRNDGEDSVRTQVTFEPLDLSYRKVSTLQNGRS 840

QY 841 QRSWRLACESASSTEVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASIGNKLLKA 900
DB 841 QRSWRLACESASSTEVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASIGNKLLKA 900
QY 901 NVTSENMPRTNKTEFQLELPVKYAVVMVVTSHGVSTKYLNFTASENTRVWQHVOYQVSN 960
DB 901 NVTSENMPRTNKTEFQLELPVKYAVVMVVTSHGVSTKYLNFTASENTRVWQHVOYQVSN 960
QY 961 LQORSLPISLVFLVPVRLNQTVIWDPRQVTFSENLSSSTCHTKERLPSSHSDFLAELRKAPV 1020
DB 961 LQORSLPISLVFLVPVRLNQTVIWDPRQVTFSENLSSSTCHTKERLPSSHSDFLAELRKAPV 1020
QY 1021 VNCISAVCQRIQCDIPFFGIOEENFATLKNLSDPDWYIKTSHNHLIIIVSTABILFNDVSF 1080
DB 1021 VNCISAVCQRIQCDIPFFGIOEENFATLKNLSDPDWYIKTSHNHLIIIVSTABILFNDVSF 1080
QY 1081 TLLPGQAGFVRSQETKVEPEVNPPLIIVGSSVGGLLLLALITAAALYKLGFFKQRYKD 1140
DB 1081 TLLPGQAGFVRSQETKVEPEVNPPLIIVGSSVGGLLLLALITAAALYKLGFFKQRYKD 1140
QY 1141 MWSEGGPPGAEPQ 1153
DB 1141 MWSEGGPPGAEPQ 1153

RESULT 5
AA014428
ID AA014428 standard; protein; 1153 AA.
XX AA014428;
AC AA014428;
DT 03-MAY-2002 (first entry)
XX Integrin Mac-1 alpha subunit.
DE Mac-1; integrin alpha subunit; variant integrin inserted domain protein;
KW open conformation; integrin related inflammatory disorder;
KW integrin related immunological disorder; rheumatoid arthritis; ischaemia;
KW reperfusion; hypovolemic shock; infarction; cerebral shock;
KW viral infection; cancer; gene therapy; vaccine;
KW bioactive agent screening.
OS Unidentified.
XX WO200204521-A2.
XX 17-JAN-2002.
XX 09-JUL-2001; 2001WO-US021805.
XX 07-JUL-2000; 2000US-0216600P.
XX (CALY) CALIFORNIA INST OF TECHNOLOGY.
XX (BLOO-) CENT BLOOD RES.
XX Springer T;
XX WPI; 2002-148167/19.
XX New integrin I domain protein having alteration in at least 2
XX noncontiguous regions and exits in an open conformation, useful for
XX treating, preventing or suppressing inflammatory or immunological
XX disorders.
XX Example 1; Fig 1F; 90pp; English.
XX The invention comprises structurally biased variant integrin inserted (I)
XX domain proteins, wherein the alterations to the protein occur in at least
XX two noncontiguous regions. Specifically the variant integrin I domain
XX proteins are structurally biased to exist in the open conformation.
XX thereby altering the binding ability of the protein. The invention also
XX comprises nucleic acids encoding the variant integrin I domain proteins.

CC The integrin I domain proteins and nucleic acids are useful for treating,
CC preventing or suppressing integrin related inflammatory and immunological
CC disorders (e.g. rheumatoid arthritis). The variant integrin I domain
CC proteins and nucleic acids can also be used for treating: ischaemia/
CC reperfusion (e.g. hypovolemic shock); infarction; cerebral shock; viral
CC infection; and cancer. The variant integrin I domain nucleic acids and
CC proteins may be used in gene therapy, as vaccines and to screen for
CC bioactive agents. The present amino acid sequence represents the Mac-1
CC alpha subunit of integrin
XX
SQ Sequence 1153 AA;

Query Match 100.0%; Score 5953; DB 5; Length 1153;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALRVLLLTALTLCHGFNLDTENAMTFQENARGQSVVQLQGRVVGAPQEIIVANQR 60
DB 1 MALRVLLLTALTLCHGFNLDTENAMTFQENARGQSVVQLQGRVVGAPQEIIVANQR 60
QY 61 GSLVQCDYSTGSCPIRLQVPEAVNMSLGLSLAATSPPLLACGPTVHQTCSNTYVK 120
DB 61 GSLVQCDYSTGSCPIRLQVPEAVNMSLGLSLAATSPPLLACGPTVHQTCSNTYVK 120
QY 121 GLCFLFGSLNRQPKPEALRGCPQEDSDIAFLIDGSGSIIPHDFRMKEFVSTVMEQL 180
DB 121 GLCFLFGSLNRQPKPEALRGCPQEDSDIAFLIDGSGSIIPHDFRMKEFVSTVMEQL 180
QY 181 KKSXTLSLMQYSEFRHFTHFKFQNNPNRSLVKPTITQLLGRTHATGIRKVVRELFN 240
DB 181 KKSXTLSLMQYSEFRHFTHFKFQNNPNRSLVKPTITQLLGRTHATGIRKVVRELFN 240
QY 241 ITNGARKNAFKILVITDGEFGDPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQEL 300
DB 241 ITNGARKNAFKILVITDGEFGDPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQEL 300
QY 301 NTIASKPRDRHVQVNNFEALKTIONLREKXFAIEGTQTGSSSFHEMSQEGFSAIT 360
DB 301 NTIASKPRDRHVQVNNFEALKTIONLREKXFAIEGTQTGSSSFHEMSQEGFSAIT 360
QY 361 SNGPLSTVGSYDAGGVFLYTSKEKSTFINWTRVDSMDNDAYLGYAAIILNRVQSLV 420
DB 361 SNGPLSTVGSYDAGGVFLYTSKEKSTFINWTRVDSMDNDAYLGYAAIILNRVQSLV 420
QY 421 LGAPRYQHIGLVAMFRONTGWESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLVIGAP 480
DB 421 LGAPRYQHIGLVAMFRONTGWESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLVIGAP 480
QY 481 HYYEQTRGGQVSVCLPRGQARWQCDAVLVYGEQGPWGRFGAALTVLGDVNGDKLTDVA 540
DB 481 HYYEQTRGGQVSVCLPRGQARWQCDAVLVYGEQGPWGRFGAALTVLGDVNGDKLTDVA 540
QY 541 IGARPEEDNRGANVLFHGTSGSGISPHSQRISAGSKLSPRLOYFGOSLGGQDITMDGLV 600
DB 541 IGARPEEDNRGANVLFHGTSGSGISPHSQRISAGSKLSPRLOYFGOSLGGQDITMDGLV 600
QY 601 DLTVGAQGHVLLRSQPLRVKAMEFNPREVARNVPCNDQVVKREAGVVRVCLHVQK 660
DB 601 DLTVGAQGHVLLRSQPLRVKAMEFNPREVARNVPCNDQVVKREAGVVRVCLHVQK 660
QY 661 STRDLREGQIQSVVYTDALDLSGRPHSRVAFNETKNSRQTQVLGLTQTCETLKLQLP 720
DB 661 STRDLREGQIQSVVYTDALDLSGRPHSRVAFNETKNSRQTQVLGLTQTCETLKLQLP 720
QY 721 NCIEDPVSPIVLRNLSLVGTPLSAFGLNLRVLAEDAQRLETFALPPEKNCNDNICDD 780
DB 721 NCIEDPVSPIVLRNLSLVGTPLSAFGLNLRVLAEDAQRLETFALPPEKNCNDNICDD 780
QY 781 LSIITFSFMSLDCLVVGGPREFNVTVVRNDCGEDSYRTOVTFFFLDLSYRKVSTLQNRS 840
DB 781 LSIITFSFMSLDCLVVGGPREFNVTVVRNDCGEDSYRTOVTFFFLDLSYRKVSTLQNRS 840
QY 841 QRSWRLACESASSTEVSGALKSTSCSINHPIFPENSEVTNITFDVDSKASLGNKLLKA 900

DB 841 QRSWRLACESASSTEVSGALKSTSCSINHPIFPENSEVTNITFDVDSKASLGNKLLKA 900
QY 901 NVTSENMPRTNKTEFOLELPVKYAVVMVTSHGVTSKYLNFTASENTSRVMOHQYQVSN 960
DB 901 NVTSENMPRTNKTEFOLELPVKYAVVMVTSHGVTSKYLNFTASENTSRVMOHQYQVSN 960
QY 961 LGQRSLPISLVFLVPLVRLNQTVIWDPRQVTFPSENLSSTCTKRLPSHSDFLAELRKAPV 1020
DB 961 LGQRSLPISLVFLVPLVRLNQTVIWDPRQVTFPSENLSSTCTKRLPSHSDFLAELRKAPV 1020
QY 1021 VNCISAVCQRIQCDIPFFGQIEEFNATLKGNLSPDWYIKTSHNHLILVSTAEILFNDSVP 1080
DB 1021 VNCISAVCQRIQCDIPFFGQIEEFNATLKGNLSPDWYIKTSHNHLILVSTAEILFNDSVP 1080
QY 1081 TLLPGQAGAFVRSQETKVEPEVNPPLIVGVSSVGGLLILALITAAALYKLGFFKROYKD 1140
DB 1081 TLLPGQAGAFVRSQETKVEPEVNPPLIVGVSSVGGLLILALITAAALYKLGFFKROYKD 1140
QY 1141 MMSEGGPPGAEPPQ 1153
DB 1141 MMSEGGPPGAEPPQ 1153
RESULT 6
ADD25615
ID ADD25615 standard; protein; 1153 AA.
XX AC ADD25615;
XX DT 15-JAN-2004 (first entry)
XX Binding domain-immunoglobulin fusion protein-associated protein #85.
XX Binding domain; immunoglobulin; fusion protein; cytostatic;
XX antiarthritic; immunosuppressive; antidiabetic; antichyroid;
XX neuroprotective; hinge region; immunoglobulin heavy chain;
XX CH2 constant region; CH3 constant region; IgG1;
XX antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
XX rheumatoid arthritis; B-cell disorder; melanoma; carcinoma; sarcoma;
XX type I diabetes mellitus; multiple sclerosis; autoimmune disease.
XX Unidentified.
XX OS US2003118592-A1.
XX PN 26-JUN-2003.
XX FD 25-JUL-2002; 2002US-00207655.
XX PF 17-JAN-2001; 2001US-0367358P.
XX PR 17-JAN-2002; 2002US-00053530.
XX PR 03-JUN-2002; 2002US-0385691P.
XX PA (GENE-) GENE-CRAFT INC.
XX PI Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
XX WPI; 2003-801317/75.
XX New binding domain-immunoglobulin fusion protein, useful for treating a
XX subject having or suspected of having a malignant condition or a B-cell
XX disorder, e.g. melanoma, Grave's disease or autoimmune disease.
XX Disclosure; SEQ ID NO 176; 157pp; English.
XX The invention relates to a binding domain-immunoglobulin fusion protein
XX comprising a binding domain polypeptide that is fused to an
XX immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain
XX CH2 constant region polypeptide that is fused to the hinge region
XX polypeptide, and an immunoglobulin heavy chain CH3 constant region
XX polypeptide that is fused to the CH2 constant region polypeptide. The

hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide contains 2 cysteine residues, where the first cysteine is not mutated; a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues, where the mutated human IgG1 immunoglobulin hinge region polypeptide contains no more than one cysteine residue; and a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide contains no cysteine residues. The binding domain-immunoglobulin fusion protein is capable of at least one immunological activity comprising antibody dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The binding domain polypeptide is capable of specifically binding to an antigen. Also included are an isolated polynucleotide encoding the binding domain-immunoglobulin fusion protein, a recombinant expression construct comprising the polynucleotide (operably linked to a promoter), a host cell transformed or transfected with a recombinant expression construct, producing the binding domain-immunoglobulin fusion protein, a pharmaceutical composition comprising the binding domain-immunoglobulin fusion protein or polynucleotide and a carrier, and treating a subject having or suspected of having a malignant condition or a B-cell disorder. The binding domain-immunoglobulin fusion protein is useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis, myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple sclerosis or autoimmune disease. The present sequence is a binding domain -immunoglobulin fusion protein-associated protein sequence. Note: The sequence data for this patent formed part of the printed specification and is also available in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?docid=20030118592. The authors have not identified the sequences in the printed specification by their SEQ ID number therefore none of the sequences can be explicitly identified.

Sequence 1153 AA;

Query Match 100.0%; Score 5953; DB 7; Length 1153;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALRVLLLTALTLCHGFNLDENAMTFQENARGFGQSVVQLQSGRVVVGAPQEIIVAAQR 60
 DB 1 MALRVLLLTALTLCHGFNLDENAMTFQENARGFGQSVVQLQSGRVVVGAPQEIIVAAQR 60
 QY 61 GSLYQCDYSTGSCPIRLQVPVEAVNMSLGLSLAATSPQALLACGPTVHTQCSNTYVK 120
 DB 61 GSLYQCDYSTGSCPIRLQVPVEAVNMSLGLSLAATSPQALLACGPTVHTQCSNTYVK 120
 QY 121 GLCFLFGNLRQOPKQPFPEALRGCPQEDSDIAFLIDGSGSIIPHDPRMKBFVSTMEOQL 180
 DB 121 GLCFLFGNLRQOPKQPFPEALRGCPQEDSDIAFLIDGSGSIIPHDPRMKBFVSTMEOQL 180
 QY 181 KSKTFLSLMOYSEFRTHFTKFPQNNPNSRLVKPIITQLGRTHATGIRKVVRELPN 240
 DB 181 KSKTFLSLMOYSEFRTHFTKFPQNNPNSRLVKPIITQLGRTHATGIRKVVRELPN 240
 QY 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVPEADREGVIRYVIGVDGAFSEKSRQEL 300
 DB 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVPEADREGVIRYVIGVDGAFSEKSRQEL 300
 QY 301 NTIASKPRDRHVQNNFEALKTIQNLREKIFAIEGTQTGSSSSFEHMSQEGFSAIT 360
 DB 301 NTIASKPRDRHVQNNFEALKTIQNLREKIFAIEGTQTGSSSSFEHMSQEGFSAIT 360
 QY 361 SNGPLLTSTVGSVDWAGGVFLYTSKEKSTFINMTRVDSMDNDAYLGYAAIILNRVQSILV 420
 DB 361 SNGPLLTSTVGSVDWAGGVFLYTSKEKSTFINMTRVDSMDNDAYLGYAAIILNRVQSILV 420
 QY 421 LCAPRYQHIGLVAMFRQNTGMWESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLIGAP 480
 DB 421 LCAPRYQHIGLVAMFRQNTGMWESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLIGAP 480

QY 481 HYYEOTRGQSVVCPPLRGQBARWQCDAVLXGEOGPKGRFGAALTVLGDVNGDKLTQVA 540
 DB 481 HYYEOTRGQSVVCPPLRGQBARWQCDAVLXGEOGPKGRFGAALTVLGDVNGDKLTQVA 540
 QY 541 IGAPCEEDNRGAVLFGHTSGSGISPSHQSQRISAGSKLSPRLQYFQGSLSGGQDLTMDGLV 600
 DB 541 IGAPCEEDNRGAVLFGHTSGSGISPSHQSQRISAGSKLSPRLQYFQGSLSGGQDLTMDGLV 600
 QY 601 DLTVGAQGHVLLLSQSPVLRVKAIMEFNPREVARNVFCNDQOVVKGKAGEVRVCLHVQK 660
 DB 601 DLTVGAQGHVLLLSQSPVLRVKAIMEFNPREVARNVFCNDQOVVKGKAGEVRVCLHVQK 660
 QY 661 STRDLREGQIQSVVTVYDLALDSGRPSRAVFNFTKSTRTQTVLGLTOTCETIKQLP 720
 DB 661 STRDLREGQIQSVVTVYDLALDSGRPSRAVFNFTKSTRTQTVLGLTOTCETIKQLP 720
 QY 721 NCIEDPVSPIVLRNFSLVGTPLSAFGLNLRPVLAEADQRLFTALFPFEKNCNDNICODD 780
 DB 721 NCIEDPVSPIVLRNFSLVGTPLSAFGLNLRPVLAEADQRLFTALFPFEKNCNDNICODD 780
 QY 781 LSITFSFMSLDCLVVGGPREFNVTVVRNDEGDSYRTQVTFPPDLDSYRKVSTLQNGRS 840
 DB 781 LSITFSFMSLDCLVVGGPREFNVTVVRNDEGDSYRTQVTFPPDLDSYRKVSTLQNGRS 840
 QY 841 QRSWLACESASTEVSGALKSTSCSINHPIFPENSEVTENITDVSQKASLGNKLLKA 900
 DB 841 QRSWLACESASTEVSGALKSTSCSINHPIFPENSEVTENITDVSQKASLGNKLLKA 900
 QY 901 NVTSENMPRTNKTEFQLELPVKYAVVMVTSKYLNTFTASENTRVVMQHOYQVSN 960
 DB 901 NVTSENMPRTNKTEFQLELPVKYAVVMVTSKYLNTFTASENTRVVMQHOYQVSN 960
 QY 961 LGQSLPISLVFLVPLVRLNQTVWDRPQVTFSENLSSTCHTKERLPSPSHDFLAELRKAPV 1020
 DB 961 LGQSLPISLVFLVPLVRLNQTVWDRPQVTFSENLSSTCHTKERLPSPSHDFLAELRKAPV 1020
 QY 1021 VNCIAVQCRIQCDIPFFGQIEEFNATLKNLSFDWYIKTSHNHLIYSTAELFNDSVF 1080
 DB 1021 VNCIAVQCRIQCDIPFFGQIEEFNATLKNLSFDWYIKTSHNHLIYSTAELFNDSVF 1080
 QY 1081 TLLPGQAFVRSQVETKVEPEVNPPLIIVGSSVGGLLALLALITAAALYKLGFFKRYKD 1140
 DB 1081 TLLPGQAFVRSQVETKVEPEVNPPLIIVGSSVGGLLALLALITAAALYKLGFFKRYKD 1140
 QY 1141 MWSEGGPPGAEPPQ 1153
 DB 1141 MWSEGGPPGAEPPQ 1153

RESULT 7
 AAR04136
 ID AAR04136 standard; protein; 1153 AA.
 XX AAR04136;
 XX 09-SEP-2004 (revised)
 DT 25-MAR-2003 (revised)
 DT 07-SEP-1990 (first entry)
 XX
 DE Alpha subunit of Mac-1 leukocyte adhesion receptor.
 XX
 KW Mac-1 alpha subunit; Mac-1 alpha/beta heterodimer;
 KW non-specific defence system; integrin gene superfamily.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 1..16
 FT /label= signal_peptide
 FT Modified-site 86..88
 FT /label= putative N-glycosylation site
 FT Modified-site 240..242
 FT /label= putative N-glycosylation site
 FT

FT	Modified-site	391..393	/label= putative N-glycosylation site
FT	Modified-site	469..471	/label= putative N-glycosylation site
FT	Modified-site	693..695	/label= putative N-glycosylation site
FT	Modified-site	697..699	/label= putative N-glycosylation site
FT	Modified-site	735..737	/label= putative N-glycosylation site
FT	Modified-site	802..804	/label= putative N-glycosylation site
FT	Modified-site	881..883	/label= putative N-glycosylation site
FT	Modified-site	901..903	/label= putative N-glycosylation site
FT	Modified-site	912..914	/label= putative N-glycosylation site
FT	Modified-site	941..943	/label= putative N-glycosylation site
FT	Modified-site	947..949	/label= putative N-glycosylation site
FT	Modified-site	979..981	/label= putative N-glycosylation site
FT	Modified-site	994..996	/label= putative N-glycosylation site
FT	Modified-site	1022..1024	/label= putative N-glycosylation site
FT	Modified-site	1045..1047	/label= putative N-glycosylation site
FT	Modified-site	1051..1053	/label= putative N-glycosylation site
FT	Modified-site	1076..1078	/label= putative N-glycosylation site
FT	Region	1106..1134	/label= putative_transmembrane_region
XX	EP364690-A.		
XX	25-APR-1990.		
XX	17-AUG-1989;	89EP-00115159.	
XX	23-AUG-1988;	88US-00235353.	
XX	09-MAR-1989;	89US-00321239.	
XX	(DAND)	DANA FARBER CANCER INST INC.	
XX	Springer TA, Corbi A;		
XX	WPI; 1990-125938/17.		
XX	N-PSDB; AAQ04043.		
XX	New pure Mac-1 alpha sub-unit and corresp. DNA - useful for treating inflammation and viral infections, and in diagnosis.		
XX	Disclosure; Page ?; 3pp; English.		
XX	Mac-1 alpha subunit is involved in the response to inflammation, i.e. recognition of and migration to sites of inflammation. It also attaches to cellular substrates as part of this function making it useful in visualising endothelial tissue. Mac-1 is a member of the Integrin Gene superfamily. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA field.)		
XX	Revised record issued on 09-SEP-2004 : Correction to feature table key and pages		
XX	Sequence 1153 AA;		
XX	Query Match	99.8%;	Score 5943; DB 2; Length 1153;
XX	Best Local Similarity	99.8%;	Pred. No. 0;
XX	Matches 1151; Conservative	1; Mismatches	1; Indels 0; Gaps

Qy	1081	TLFPQCGAFVRSQTETKVEPEVNPPLIIVGSSVGGLLLLALITAAIYKLGFFKQYKD	1140
Db	1081	TLFPQCGAFVRSQTETKVEPEVNPPLIIVGSSVGGLLLLALITAAIYKLGFFKQYKD	1140
Qy	1141	MMSEGGPPGAEPPQ	1153
Db	1141	MMSEGGPPGAEPPQ	1153
RESULT 8			
AD	ADMG9589		
ID	ADMG9589	standard; protein; 1152 AA.	
XX	XX		
AC	ADMG9589;		
XX	XX		
DT	17-JUN-2004	(first entry)	
XX	XX		
DE	Human integrin alphaM subunit precursor protein.		
XX	XX		
KW	integrin alpha subunit; beta; antipsoriatic; thrombolytic; anticoagulant;		
KW	osteopathic; cystostatic; immunosuppressive; antiinflammatory;		
KW	neuroprotective; antisticking; immunotherapy; inflammatory;		
KW	autoimmune disorder; thrombosis; cancer; osteoporosis;		
KW	sickle cell anaemia; psoriasis; multiple sclerosis; human; precursor;		
KW	alphaM.		
XX	XX		
OS	Homo sapiens.		
XX	XX		
FH	Key	Location/Qualifiers	
FT	Misc-difference 965	/note= "Encoded by CCC"	
XX	XX		
PN	WO2004007530-A2.		
XX	XX		
PD	22-JAN-2004.		
XX	XX		
PF	17-JUL-2003; 2003WO-US022301.		
XX	XX		
PR	17-JUL-2002; 2002US-0396783P.		
PR	17-JUL-2002; 2002US-0396790P.		
PR	11-SEP-2002; 2002US-0410135P.		
XX	XX		
PA	(BLOO-) CENT BLOOD RES INC.		
XX	XX		
PI	Springer TA, Takagi J;		
XX	XX		
DR	WPI; 2004-122877/12.		
XX	N-PSDB; ADM9588.		
PT	Novel modified integrin protein having extracellular domains of integrin		
PT	alpha and beta subunits or integrin alphaII and beta3 subunit, useful for		
PT	treating integrin mediated disorders.		
XX	XX		
PS	Disclosure; SEQ ID NO 4; 232pp; English.		
XX	XX		
CC	The invention relates to a novel isolated or recombinant modified		
CC	integrin protein having extracellular domains of integrin alpha and beta		
CC	subunits where one of the subunits has one or more mutations, an altered		
CC	surface feature or an amino acid substitution or internal deletion,		
CC	extracellular domains of the integrin beta subunit that comprise a		
CC	mutation that alters a non-cysteine residue to cysteine or extracellular		
CC	domains of integrin alpha and beta subunits. The polypeptide of the		
CC	invention demonstrates antipsoriatic, thrombolytic, anticoagulant,		
CC	osteopathic, cystostatic, immunosuppressive, antiinflammatory,		
CC	neuroprotective and antisticking activities and may be useful for		
CC	immunotherapy in order to prevent or treat an integrin-mediated disorder		
CC	such as an inflammatory disorder, an autoimmune disorder, thrombosis,		
CC	cancer, osteoporosis, sickle cell anaemia, psoriasis and multiple		
CC	sclerosis. The current sequence is that of the human integrin alphaM		
CC	subunit precursor protein of the invention.		
XX	XX		
SQ	Sequence 1152 AA;		

Db 1020 VNC5IAVCQRIQCDIPFFGQIEEFNATLKGNSLFDWYIKTSHNLLIVSTAELFNDVSF 1079
 Qy 1081 TLLPGGAFVRSOTETKVEPFPVNPPLPLIVGSSVGGLLLLALITAALYKLGFFKQYKD 1140
 Db 1080 TLLPGGAFVRSOTETKVEPFPVNPPLPLIVGSSVGGLLLLALITAALYKLGFFKQYKD 1139
 Qy 1141 MMSEGGPPGAEQ 1153
 Db 1140 MMSEGGPPGAEQ 1152

RESULT 9
 ADP12435
 ID ADP12435 standard; protein; 1152 AA.
 AC ADP12435;
 XX 12-AUG-2004 (first entry)
 DT Protein encoded by mRNA of the invention #45.
 DE
 DE
 XX transplant rejection; immune system; rheumatoid arthritis; lupus;
 KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
 XX
 OS Homo sapiens.
 XX
 XX WO2004042346-A2.
 PN
 PD 21-MAY-2004.
 XX
 XX 24-APR-2003; 2003WO-US012946.
 PF
 XX 24-APR-2002; 2002US-00131831.
 PR 20-DEC-2002; 2002US-00325899.
 XX
 XX (EXPR-) EXPRESSION DIAGNOSTICS INC.
 PA
 XX Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
 PI Rosenberg S;
 XX WPI; 2004-400724/37.
 DR
 XX
 PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
 PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
 PT rejection, in an individual, comprises detecting the expression level of
 PT the genes.
 XX
 PS Claim 65; SEQ ID NO 2444; 1762pp; English.
 XX
 CC The present invention relates to diagnosing or monitoring transplant
 CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
 CC comprises detecting the expression level of one or more genes. The
 CC methods, system and kits are useful in diagnosing or monitoring
 CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
 CC islet, lung, bone marrow or stem cell transplant rejection,
 CC xenotransplant rejection or mechanical organ replacement rejection, in an
 CC individual. The method is also useful in assessing the immune status of
 CC an individual. The methods are also useful in diagnosing and monitoring
 CC diseases that involve the immune system, e.g. rheumatoid arthritis,
 CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
 CC viral, bacterial or fungal infection. The present sequence represents a
 CC protein that is encoded by the mRNA of the invention.
 XX
 SQ Sequence 1152 AA;

Query Match 99.6%; Score 5930.5; DB 8; Length 1152;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1150; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 MAURVLLTALTCHGNLDTENAMTFOENARGQSVQVQGSRRVVVGAPQEIVAAQR 60
 Db 1 MAURVLLTALTCHGNLDTENAMTFOENARGQSVQVQGSRRVVVGAPQEIVAAQR 60

Qy 61 GSLVQCDYSTSCBPIRLQVPVEAVNMISLGLSLAATTSPPQLLACGPTVHOTCSENTYVK 120
 Db 61 GSLVQCDYSTSCBPIRLQVPVEAVNMISLGLSLAATTSPPQLLACGPTVHOTCSENTYVK 120
 Qy 121 GLCFLFGSNLQOQPKPEALRGCPQEDSDIAFLIDGSGSII PHDFRMRKMFVSTVMEQL 180
 Db 121 GLCFLFGSNLQOQPKPEALRGCPQEDSDIAFLIDGSGSII PHDFRMRKMFVSTVMEQL 180
 Qy 181 KKSMTLFSLMQYSEBFRIHFTFKFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFN 240
 Db 181 KKSMTLFSLMQYSEBFRIHFTFKFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFN 240
 Qy 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVI PEADREGVIRYVIGVGDARSEKSRQEL 300
 Db 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVI PEADREGVIRYVIGVGDARSEKSRQEL 300
 Qy 301 NTIASKPPRDHVFQNNFEALKTIONLRKXKFAIEGTQTGSSSSFEHEMSQEGFSAAIT 360
 Db 301 NTIASKPPRDHVFQNNFEALKTIONLRKXKFAIEGTQTGSSSSFEHEMSQEGFSAAIT 360
 Qy 361 SNGPLLSTVGSYDWAGGVFLYTSKEKSTFINNTRVDSMDNDAYLYGAAAIIILNRVQSLV 420
 Db 361 SNGPLLSTVGSYDWAGGVFLYTSKEKSTFINNTRVDSMDNDAYLYGAAAIIILNRVQSLV 420
 Qy 421 LGAPRYOHIGLVAMFRONTGMWESNANVKGTOIGAYFCASICSVDVDSNGSTDVLIGAP 480
 Db 421 LGAPRYOHIGLVAMFRONTGMWESNANVKGTOIGAYFCASICSVDVDSNGSTDVLIGAP 480
 Qy 481 HYTEQTRGGQVSVCPPLPRGQARWQCDAVLYGEGQGPWGRFGAALTVLGDVNGDKLTDVA 540
 Db 481 HYTEQTRGGQVSVCPPLPRGQARWQCDAVLYGEGQGPWGRFGAALTVLGDVNGDKLTDVA 540
 Qy 541 IGAPGEDNRCANVLFHGTSGSGISPSHSQRIAGSKLSPRIQYFGQSLSGQDITMDGLV 600
 Db 541 IGAPGEDNRCANVLFHGTSGSGISPSHSQRIAGSKLSPRIQYFGQSLSGQDITMDGLV 600
 Qy 721 NCIEDPVSPIVLRNFSLVGTPLSAFNLRPVLAEDAQRFTALFPFEKNCNDNI CODD 780
 Db 721 NCIEDPVSPIVLRNFSLVGTPLSAFNLRPVLAEDAQRFTALFPFEKNCNDNI CODD 780
 Qy 781 LSITFSFMSLDCLVVGPFREFNVTVTVRNDGEDSYRTQVTFPPFDLSYRKVSTLQNRS 840
 Db 781 LSITFSFMSLDCLVVGPFREFNVTVTVRNDGEDSYRTQVTFPPFDLSYRKVSTLQNRS 840
 Qy 841 QRSWLACESASSTEVSGALKSTSCSINHPIPPENSEVTNITFDVDSKASLGNKLLKA 900
 Db 841 QRSWLACESASSTEVSGALKSTSCSINHPIPPENSEVTNITFDVDSKASLGNKLLKA 900
 Qy 901 NVTSENNMPNTKTEFOLELPVKYAVVMVVTSHGVSTKYLNFTASENTSRVMQHOYQVSN 960
 Db 901 NVTSENNMPNTKTEFOLELPVKYAVVMVVTSHGVSTKYLNFTASENTSRVMQHOYQVSN 960
 Qy 961 LGQRSPPISLVFLVPLVRLNQTIVDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPV 1020
 Db 961 LGQRSPPISLVFLVPLVRLNQTIVDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPV 1020
 Qy 1021 VNC5IAVCQRIQCDIPFFGQIEEFNATLKGNSLFDWYIKTSHNLLIVSTAELFNDVSF 1080
 Db 1020 VNC5IAVCQRIQCDIPFFGQIEEFNATLKGNSLFDWYIKTSHNLLIVSTAELFNDVSF 1079
 Qy 1081 TLLPGGAFVRSOTETKVEPFPVNPPLPLIVGSSVGGLLLLALITAALYKLGFFKQYKD 1140
 Db 1080 TLLPGGAFVRSOTETKVEPFPVNPPLPLIVGSSVGGLLLLALITAALYKLGFFKQYKD 1139

Qy 1141 MMSGGPPGABPQ 1153
Db 1140 MMSGGPPGABPQ 1152

RESULT 10
ID ADP44061 standard; protein; 1163 AA.
XX AC ADP44061;
XX DT 09-SEP-2004 (first entry)
XX DE Human CD11c protein SEQ ID NO:14.
XX KW HIV entry inhibitor; cell surface protein inhibitor; HIV infection;
XX KW anti-HIV; virucide; HIV uptake inhibitor; human; CD11c; integrin alpha x.
XX OS Homo sapiens.
XX PN WO2004053094-A2.
XX PD 24-JUN-2004.
XX PF 08-DEC-2003; 2003WO-US039208.
XX PR 06-DEC-2002; 2002US-0431522P.
XX PA (PPDP-) PPD DEV LP.
XX PI Dunn SÜ, Holzmayer TA;
XX DR WPI; 2004-480928/45.
XX DR N-PSDB; ADP44060.
XX PT Identifying an inhibitor of human immunodeficiency virus (HIV) entry into
XX PT a human host cell useful for preventing and/or treating HIV infection, by
XX PT identifying an inhibitor of a cell surface polypeptide such as CXCR-4.
XX PS Claim 1; SEQ ID NO 14; 133pp; English.
XX CC The present invention describes a method (M1) for identifying an
XX CC inhibitor of HIV entry into a human host cell. (M1) comprises identifying
XX CC an inhibitor of a cell surface polypeptide selected from CXCR-4 (352
XX CC amino acids, SEQ ID NO:8, ADP44055), CCR4 (360 amino acids, SEQ ID NO:10,
XX CC ADP44057), CCR7 (378 amino acids, SEQ ID NO:12, ADP44059), CD11c (1163
XX CC amino acids, SEQ ID NO:14, ADP44061), CD47 (323 amino acids, SEQ ID
XX CC NO:16, ADP44063), CD68 (354 amino acids, SEQ ID NO:18, ADP44065), CD69
XX CC (199 amino acids, SEQ ID NO:20, ADP44067), CD74 (366 amino acids, SEQ ID
XX CC NO:22, ADP44069), CSF3R (836 amino acids, SEQ ID NO:24, ADP44071), RARA
XX CC (462 amino acids, SEQ ID NO:26, ADP44073), GABBR1 (578 amino acids, SEQ
XX CC ID NO:28, ADP44075), P2X1 (150 amino acids, SEQ ID NO:30, ADP44077),
XX CC HELO1 (299 amino acids, SEQ ID NO:32, ADP44079), GPRK6 (576 amino acids,
XX CC SEQ ID NO:34, ADP44081), or PFK2B (1009 amino acids, SEQ ID NO:36,
XX CC ADP44083). Also described: (1) an inhibitor of a cell surface polypeptide
XX CC as described above in a human host cell preventing HIV entry into the
XX CC human host cell; (2) a pharmaceutical composition comprising an inhibitor
XX CC of (1) and a carrier; and (3) conferring resistance to HIV infection in
XX CC an individual, by administering the pharmaceutical composition of (2). An
XX CC inhibitor of HIV entry has anti-HIV and virucide activities, and can be
XX CC used as an HIV uptake inhibitor. (M1) is useful for identifying
XX CC protective compounds that inhibit entry of HIV into cells, useful for the
XX CC prevention and/or treatment of HIV infection. The present sequence
XX CC represents human integrin alpha x (CD11c), which is used in the
XX CC exemplification of the present invention.

Qy 5 VLLLTALTLCHGFLNLTENAMTFQENARGFGQSVVQLQGSRRVVVGAPQEIIVAAVNRQSLY 64

Db 8 LLLFTALATSLGFLNLTDELTAFRVDSAGFGSDSVVQVANSVWVVGAPQKITAANQTGGLY 67
Qy 65 QDYSTGSCBPIRLQVPVEAVNMSLGLSLAATTSPQLLACGPTVHOTCSENTYVKGICF 124
Db 68 QCGYSTGACEFGLQVPPPEAVNMSLGLSLASTTSPQLLACGPTVHHCGRNMYITGLCF 127
Qy 125 LFGSNLRQOQKQFPPEALRGCPQEDSDIAFLDGSIIIPHDFFRRMKFVSTVMEQLKSK 184
Db 128 LLGPT--QLTQRLPVSQRQECPRQBDIVFLIDGSGSISSRNFAFMNFWRAVISQFQPS 185
Qy 185 TLPSLMQYSEBFRJHFTFKFQNNPNRSLVKPTTOLLGRTHTATGIRKVVRELENYING 244
Db 186 TQPSLMQFSNKFQTHFTFEFRSSNPLSLASVHQLQGFYTTATAIQVNVHRLPHASVG 245
Qy 245 ARKNAKILVITDGEKFGDPLGYEDVIPEDREGVIRYVIGVGDFAFSEKSRQELNTIA 304
Db 246 ARRAAKILVITDGEKFGDPLGYEDVIPEDREGVIRYVIGVGDFAFSEKSRQELNTIA 305
Qy 305 SKPPRDHVFQVNFPEALKTIQNLREKXFAIEGTQTGSSSFEHBMSEGEFSAATISNGP 364
Db 306 SKPSQEHIFKVEDFDALKDIQNLKEKIFAIEGTETTSSSFELEMAQEGFSAVTPDGP 365
Qy 365 LLSTVGSYDNAGCVFLYTSKEKSTFNNTRVDSMDNDAYLGYAAAIILNRVQSLVIGAP 424
Db 366 VLGAVGSFTWSGGAFLYPPNMSPTFINMSQENVDMDSDSYLSTELALWKVQSLVLGAP 425
Qy 425 RYQHIGLVAMFRONTGMWESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLIGAPHYYE 484
Db 426 RYQHTGRAVIFTQVSRQWRKAEVTGTOIGYFGASLCSVDVDSNGSTDVLIGAPHYYE 485
Qy 485 QTRGGQVSVCELPGRQARWQCDVALYGEQOQPMGRFGAALTVLGDVNGDKLTDVAIGAP 544
Db 486 QTRGGQVSVCELPGRWR--RWCDAVLYGEQGHMGRFGAALTVLGDVNGDKLTDVVGAP 544
Qy 545 GEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGSLGSGGDLTWGDLVDTLV 504
Db 545 GEENRGAVYLFHGVLGPSISPSHSQRIAGSKLSPRLQYFGSLGSGGDLTWGDLVDTLV 604
Qy 605 GAQGHVLLLRQSPVLRVKAIMEFNPREVARNVFCNDQVWVGKEAGEVRVCLHVOKSTRD 664
Db 605 GARQVLLLRTRPVLWVGVSNOQFPAEIPRAFAFCEQVSEQTLVQSNICLYIDKRSKN 664
Qy 665 RLREGQIQSVVYDLDLDSGRPHRAVFNETKNSRTRQTVLGLTQTCETLKLQLPNCIE 724
Db 665 LLSRDLQSSVTLDLADPGRLSPRATFOETKNRSLSRVRVLGLKAHCENFNLLPSCVE 724
Qy 725 DPVSPVLRNFSLVGTPLSAFGLNRPVLAEDAQLFTALPFEKNCNDNICODDLSIT 784
Db 725 DSVTPITLRLNFTLVGLPELLAFRLRPLAADAQRYFTASLPFEKNCADHICQDNLGIS 784
Qy 785 FSNMSLCLVVGPGREFNVTVVRNDGSDSVYRTVTPFPFLDLSYRKVSTLQNRQSRWS 844
Db 785 FSPFLKSLVVGSLNELNAEVMVWVNDGSDSVYRTVTPFPFLDLSYRKVSTLQNRQSRWS 844
Qy 845 PLACESASTSVGALKSTSCSINHPIPEENSEVFNITFDVDSKASLGNKLLKANVTS 904
Db 845 HLTCDSDAPVG--SQGTWSTSCRINHLIPRGGAQITFLATFDVSPKAVLGDRLLLTANVSS 902
Qy 905 ENNPRNTKTFQELPVLKYAVYVTVSHGVSTKVLNFTAS--ENTSRVWQHOYVSNLQ 963
Db 903 ENNPTKSTKTFQELPVLKYAVYVTVSHGVSTKVLNFTAS--ENTSRVWQHOYVSNLQ 962
Qy 964 RSLPISLVFLVPLRNLQTVIWDPRQVTFSENLSSSTCHTKERLPSHSDFLAEILKAPVWNC 1023
Db 963 RDLPVSNFVFWPVELNQAEMVMDVEVSHVPQPSLRCSSEKTAAPPASDFLAHQKPVLD 1022
Qy 1024 SIACVQRIQCDIPFFGIEEFNATLKGNSLDFWYIKTSHNHLIIVSTAEILFNDSVFTLL 1083
Db 1023 SIAGCLRPRCDVPSPVQBELDFTLKGNSLFGWVRQILQKKVSVVSVVAEITFDTSVYSOL 1082
Qy 1084 PQGAFVRSQVETKVEPEFVFNPLIYVSSVGGLLILALITAAALYKLGFFPKQVYKDWMS 1143

XX DE Human soft tissue sarcoma-upregulated protein - SEQ ID 327.
XX KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
XX OS Homo sapiens.
XX FN WO2004048938-A2.
XX PD 10-JUN-2004.
XX PF 26-NOV-2003; 2003WO-US038193.
XX PR 26-NOV-2002; 2002US-0429739P.
XX PA (PROT-) PROTEIN DESIGN LABS INC.
XX PI Aziz N, Ginsburg WM, Zlotnik A;
XX DR WPI; 2004-441208/41.
XX PT Early detection of soft tissue sarcoma comprises determining expression
XX PT of a gene in a first soft tissue sample and a normal soft tissue sample
XX PT and comparing the gene expression, also useful in treating soft tissue
XX PT sarcoma.
XX PS Example 2; SEQ ID NO 327; 210pp; English.
XX CC The invention relates to a novel method for detecting soft tissue sarcoma
XX CC which comprises obtaining a first soft tissue sample from an individual
XX CC and a normal soft tissue sample from the same or different individual,
XX CC determining the expression of a gene in both samples and comparing the
XX CC expression of the gene in both soft tissue samples, where a higher level
XX CC of protein expression in the first soft tissue sample indicates the
XX CC presence of soft tissue sarcoma. The method of the invention has
XX CC cytotatic applications and may be useful for detecting soft tissue
XX CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
XX CC acid sequences may be useful in diagnostic and screening applications.
XX CC The current sequence is that of a human soft tissue sarcoma-upregulated
XX CC protein of the invention. The current sequence is not shown within the
XX CC specification per se but was submitted in CD format by the inventor.
XX SQ Sequence 1163 AA;
Query Match 58.8%; Score 3500; DB 8; Length 1163;
Best Local Similarity 61.3%; Pred. No. 2e-277;
Matches 599; Conservative 139; Mismatches 297; Indels 6; Gaps 4;
QY 5 VLLTALTLCHGFNLDENAMTFQENARFGQSVVQLQGSRRVVGAPQEIIVAAANQRGSLY 64
DB 8 LLLFTALATSLGFLNLDTELTAFRVDSAGFGDSVVQYANWVVGAPQKITAANQTGGLY 67
QY 65 QCDYSTGCEPIRLQVPEAVNMSLGLSIAATSPOLLACGPTVHTCSENTYVKGLCF 124
DB 68 QCGYSTGACEPIGLQVPEAVNMSLGLSIAATSPOLLACGPTVHTCSENTYVKGLCF 127
QY 125 LFGSNLRQPOKFPBALGCGPOEDSIAFLIDGSGIIPHPFRMKFVSTVMEOLKKSX 184
DB 128 LLGPT--QLTQLPVSRQECRQEQDIIVLIDGSGISIRNFATMNFVRAVISQFQPS 185
QY 185 TLFSLMYSSEFRHFTFKGFQNNPNRSLVKPITQLLGRTHATGIRKVRVRELNIYNG 244
DB 186 TQFSLMQFSNKPQTHFTFEFRRTSNPLSLASVHQLQGFYTTATAIQNVHRLPHASVG 245
QY 245 ARKNAFKILVITDCEKGDPLGYEDVTPADREGVIRYVGVGDAFRSEKSRQELNTIA 304
DB 246 ARRDATKILVITDCKGSDLDYDVTIPMDAAGIIRIYAGVGLAFQNRNSWKELNDIA 305
QY 305 SKPPRDHVFQVNNFEALKTIQNLREKXFAIBGTOTGSSSSPEHEMSQEGFAAITSNGP 364
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XX AC AAR07120;
XX DT 25-MAR-2003 (revised)
XX DT 05-FEB-1991 (first entry)
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XX p150.95 leucocyte adhesion receptor alpha-subunit; hairy cell leukaemia;
XX rhinovirus.
XX OS Synthetic.
XX PH Key Location/Qualifiers

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2005, 15:13:36 ; Search time 190.522 Seconds
(without alignments)
2186.449 Million cell updates/sec

Title: RWHULB-A

Perfect score: 5953

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Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	5953	100.0	1153	10	US-09-902-481A-1
3	5953	100.0	1153	10	US-09-891-943-3
4	5953	100.0	1153	14	US-10-144-259-30
5	5953	100.0	1153	14	US-10-207-655-176
6	5937.5	99.7	1152	9	US-09-945-265-4
7	5865	98.5	1137	10	US-09-902-481A-6
8	5859	98.4	1137	10	US-09-902-481A-5
9	5849	98.3	1137	10	US-09-902-481A-4
10	5836	98.0	1137	10	US-09-902-481A-3
11	3500	58.8	1163	14	US-10-116-275-204
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14	3477	58.4	1163	10	US-09-891-943-4	Sequence 4, Appli
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17	3436.5	57.7	1161	9	US-09-350-259-99	Sequence 99, Appl
18	3436.5	57.7	1161	10	US-09-891-943-99	Sequence 99, Appl
19	3261	54.8	1161	9	US-09-350-259-53	Sequence 53, Appl
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21	3248.5	54.6	1161	9	US-09-350-259-55	Sequence 55, Appl
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26	3194.5	53.7	1151	10	US-09-891-943-37	Sequence 37, Appl
27	1848	31.0	369	13	US-10-087-192-1212	Sequence 1212, Ap
28	1560	26.2	1170	9	US-09-945-265-2	Sequence 2, Appli
29	1556	26.2	1170	17	US-10-473-127-1743	Sequence 1743, Ap
30	1556.5	26.1	1145	17	US-10-872-198-130	Sequence 130, App
31	1556	26.1	1170	15	US-10-261-164-1	Sequence 1, Appli
32	1556	26.1	1170	17	US-10-473-127-1737	Sequence 1737, Ap
33	1556	26.1	1170	17	US-10-473-127-1739	Sequence 1739, Ap
34	1556	26.1	1170	17	US-10-473-127-1742	Sequence 1742, Ap
35	1552.5	26.1	1145	17	US-10-473-127-1738	Sequence 1738, Ap
36	1532.5	25.7	1223	16	US-10-408-765A-295	Sequence 295, App
37	1532.5	25.7	1223	17	US-10-473-127-1736	Sequence 1736, Ap
38	1462	24.6	1086	17	US-10-473-127-1741	Sequence 1741, Ap
39	1443.5	24.2	1065	17	US-10-473-127-1740	Sequence 1740, Ap
40	1358	22.8	1086	16	US-10-408-765A-1871	Sequence 1871, Ap
41	1358	22.8	1086	17	US-10-473-127-1735	Sequence 1735, Ap
42	1358	22.8	1086	17	US-10-473-127-1744	Sequence 1744, Ap
43	1229.5	20.7	494	9	US-09-350-259-103	Sequence 103, App
44	1229.5	20.7	494	10	US-09-891-943-103	Sequence 103, App
45	1186.5	19.9	413	9	US-09-350-259-101	Sequence 101, App

ALIGNMENTS

RESULT 1
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; Sequence 3, Application US/09350259
; Patent No. US20020062008A1
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; TITLE OF INVENTION: No. US20020062008A1el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/350,259
; CURRENT FILING DATE: 1999-07-08
; EARLIER APPLICATION NUMBER: 09/193,043
; EARLIER FILING DATE: 1998-11-16
; EARLIER APPLICATION NUMBER: 08/173,497
; EARLIER FILING DATE: 1993-12-23
; EARLIER APPLICATION NUMBER: 08/286,889
; EARLIER FILING DATE: 1994-08-05
; EARLIER APPLICATION NUMBER: 08/362,652
; EARLIER FILING DATE: 1994-12-21
; EARLIER APPLICATION NUMBER: 08/943,363
; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-350-259-3

Query Match 100.0%; Score 5953; DB 9; Length 1153;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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; Publication No. US2003005440A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy
; APPLICANT: Shimaoka, Motomu
; APPLICANT: Shifman, Julia
; APPLICANT: Mayo, Stephen
; TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
; FILE REFERENCE: A-70586-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/902.481A
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/216,600
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (17)..()
; OTHER INFORMATION:
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Best Local Similarity 99.9%; Pred. No. 0;
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; Publication No. US20030077278A1
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; TITLE OF INVENTION: Van der Vieren, Monica
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/891, 943
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 09/193,043
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/286,889
; PRIOR FILING DATE: 1994-08-05
; PRIOR APPLICATION NUMBER: 08/362,652
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/943,363
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-891-943-3

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Best Local Similarity 99.9%; Pred. No. 0;

Matches 1152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Qy 181 KKSKTLLFSLMOYSEBFRIHFTFKBPQNNPNPSLVKPIQTLGRTHATGIRKVVRELFN 240
Db 181 KKSKTLLFSLMOYSEBFRIHFTFKBPQNNPNPSLVKPIQTLGRTHATGIRKVVRELFN 240
Qy 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVIPADREGVIRYVIGVGDAFRSEKSRQEL 300
Db 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVIPADREGVIRYVIGVGDAFRSEKSRQEL 300
Qy 301 NTIASKPRDRHVQNNFEALKTIONOLREKXFAIEGTQGTSSSSFEHEMSOEGFSAALT 360
Db 301 NTIASKPRDRHVQNNFEALKTIONOLREKXFAIEGTQGTSSSSFEHEMSOEGFSAALT 360
Qy 361 SNGPLLLSTVGSYDWAAGGVFLYTSKEKSTPINMTRVDSMDNDAYLGYAAAIILNRVQSLV 420
Db 361 SNGPLLLSTVGSYDWAAGGVFLYTSKEKSTPINMTRVDSMDNDAYLGYAAAIILNRVQSLV 420
Qy 421 LGAPRYQHIGLVAMPQNTGMWESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLIGAP 480
Db 421 LGAPRYQHIGLVAMPQNTGMWESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLIGAP 480
Qy 481 HYYETRGQSVQVCPPLRGORARWOCDAVLGEQSQPMGRFGAALTVLGDVNGDKLTDVA 540
Db 481 HYYETRGQSVQVCPPLRGORARWOCDAVLGEQSQPMGRFGAALTVLGDVNGDKLTDVA 540
Qy 541 IGAPEEDNRGAVYLFHGTSGSGISPSHSQRTAGSKLSPRLQYFGQSLGGQDLTMDGLV 600
Db 541 IGAPEEDNRGAVYLFHGTSGSGISPSHSQRTAGSKLSPRLQYFGQSLGGQDLTMDGLV 600
Qy 601 DLTGGAQGHVLLRSQVLRVKAIMEFNPREVARNVFECDQVVKGEAGEVRVCLHVOK 660
Db 601 DLTGGAQGHVLLRSQVLRVKAIMEFNPREVARNVFECDQVVKGEAGEVRVCLHVOK 660
Qy 661 STRDRLEGOIQSVVTVYDIALDSGRPHSRVAVNETKNSRRQTQVGLTQTCETLKQLP 720
Db 661 STRDRLEGOIQSVVTVYDIALDSGRPHSRVAVNETKNSRRQTQVGLTQTCETLKQLP 720
Qy 721 NCIEDPVSPVILRLNFSLVGTPLSAFGLNLRPVLAEDAQRLFTALPFPEKNCNDNICQDD 780
Db 721 NCIEDPVSPVILRLNFSLVGTPLSAFGLNLRPVLAEDAQRLFTALPFPEKNCNDNICQDD 780
Qy 781 LSITFSFMSLDCLVVGGPREFNVTVTRNDGSDSYRTQVTFPPDLDSYRKVSTLQNR 840
Db 781 LSITFSFMSLDCLVVGGPREFNVTVTRNDGSDSYRTQVTFPPDLDSYRKVSTLQNR 840
Qy 841 QRSWLACSSASSTEVSGALKSTCSINHPIPFENSEVTFTNFDFVDSKASLGKLLKA 900
Db 841 QRSWLACSSASSTEVSGALKSTCSINHPIPFENSEVTFTNFDFVDSKASLGKLLKA 900
Qy 901 NVTSENNPRTNKTETFOLELPVKYAVYVTVTSHGVSTKYLNFTASENTSRVMOHQVSN 960
Db 901 NVTSENNPRTNKTETFOLELPVKYAVYVTVTSHGVSTKYLNFTASENTSRVMOHQVSN 960
Qy 961 LQORSLPISLVLVPLVRLNQTVWDRPQVTFSENLSSTCHTKERLPSSHSDFLAELRKAPV 1020
Db 961 LQORSLPISLVLVPLVRLNQTVWDRPQVTFSENLSSTCHTKERLPSSHSDFLAELRKAPV 1020
Qy 1021 VNCSTAVCQRIQCDIPFPGIQEENATLKGNSFDWYIKTSHNLLIVSTAEILFNDVSF 1080
Db 1021 VNCSTAVCQRIQCDIPFPGIQEENATLKGNSFDWYIKTSHNLLIVSTAEILFNDVSF 1080

QY 1081 TLLPGGAFVRSOTETKVEFPFVNPDLPLIVGSSVGGILLALLIITAAALYKLGFFKQYKD 1140
DB 1081 TLLPGGAFVRSOTETKVEFPFVNPDLPLIVGSSVGGILLALLIITAAALYKLGFFKQYKD 1140
QY 1141 MMSEGGPPGAEPQ 1153
DB 1141 MMSEGGPPGAEPQ 1153

RESULT 4
US-10-144-259-30
; Sequence 30, Application US/10144259
; Publication No. US20030109691A1
; GENERAL INFORMATION:
; APPLICANT: Arnaout, M. Amin
; APPLICANT: Li, Rui
; APPLICANT: Xiong, Jian-Ping
; TITLE OF INVENTION: VARIANT INTEGRIN POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 00786-548001
; CURRENT APPLICATION NUMBER: US/10/144,259
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: US 09/758,493
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/221,950
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-259-30

Query Match 100.0%; Score 5953; DB 14; Length 1153;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 1MALRVLLLTALTLCHGFNLDTENAMTFQENARGFQGVVQLOGSRVVGAPQEIIVAAANOR 60
DB 1 1MALRVLLLTALTLCHGFNLDTENAMTFQENARGFQGVVQLOGSRVVGAPQEIIVAAANOR 60
QY 61 GSLYQCDYSTGCEPIRLQVPEAVNMSLGLSLAATTPPQLLACGPTVHTCSENTYVK 120
DB 61 GSLYQCDYSTGCEPIRLQVPEAVNMSLGLSLAATTPPQLLACGPTVHTCSENTYVK 120
QY 121 GLCFLFGSNLRQOPKPEALRGCPQEDSDIAFLIDGSGSIIPHPFRMKFVSTVMSQL 180
DB 121 GLCFLFGSNLRQOPKPEALRGCPQEDSDIAFLIDGSGSIIPHPFRMKFVSTVMSQL 180
QY 181 KKSRTLFLSMQYSEEFRIHFTKPEQNNPNRSLVKPITQLIGRTHATGIRKVVRELFN 240
DB 181 KKSRTLFLSMQYSEEFRIHFTKPEQNNPNRSLVKPITQLIGRTHATGIRKVVRELFN 240
QY 241 ITNGARKNAFKLVITDGEKDPGLGVEDVPEADREGVIRYVIGVDGAPRSEKSRQEL 300
DB 241 ITNGARKNAFKLVITDGEKDPGLGVEDVPEADREGVIRYVIGVDGAPRSEKSRQEL 300
QY 301 NTIASKPRDRHVQVNNPEALKTIQNLREKXFAIEGTQTGSSSSFEHMSQEGFSAAIT 360
DB 301 NTIASKPRDRHVQVNNPEALKTIQNLREKXFAIEGTQTGSSSSFEHMSQEGFSAAIT 360
QY 361 SNGPLLTSTVGSYDAGGVFLYTSKSTFINMTRVDSMDNDAYLGYAAAILRNVRQSLV 420
DB 361 SNGPLLTSTVGSYDAGGVFLYTSKSTFINMTRVDSMDNDAYLGYAAAILRNVRQSLV 420
QY 421 LGAPRYQHIGLVAMFRONTGMWESNANVKGTQIGAYFGASLCSDVDNSGSTDVLIGAP 480
DB 421 LGAPRYQHIGLVAMFRONTGMWESNANVKGTQIGAYFGASLCSDVDNSGSTDVLIGAP 480
QY 481 HYTEQTRGGQSVCPPLPRGARWQCDVAVLGEQGPWGRFGAALTVLGDVNGDKLTDVA 540
DB 481 HYTEQTRGGQSVCPPLPRGARWQCDVAVLGEQGPWGRFGAALTVLGDVNGDKLTDVA 540

RESULT 5
US-10-207-655-176
; Sequence 176, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 176
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-176

Query Match 100.0%; Score 5953; DB 14; Length 1153;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 1MALRVLLLTALTLCHGFNLDTENAMTFQENARGFQGVVQLOGSRVVGAPQEIIVAAANOR 60
DB 1 1MALRVLLLTALTLCHGFNLDTENAMTFQENARGFQGVVQLOGSRVVGAPQEIIVAAANOR 60

QY 541 IGAPCEENRGAVLYFHGTSGLSPSHSQRISAGSKLSPRLQYFGOSLGGODLTMDGLV 600
DB 541 IGAPCEENRGAVLYFHGTSGLSPSHSQRISAGSKLSPRLQYFGOSLGGODLTMDGLV 600
QY 601 DLTVGAQGHVLLRSQPVLRVKAIMEFNPREVARNVFECDQVVKGEAGEVRVCLHVQK 660
DB 601 DLTVGAQGHVLLRSQPVLRVKAIMEFNPREVARNVFECDQVVKGEAGEVRVCLHVQK 660
QY 661 STRDLREGQIQSVVYTDIALDSCRPHSRVAFNETKNSRTRQTVLGLTQTCETLKLQLP 720
DB 661 STRDLREGQIQSVVYTDIALDSCRPHSRVAFNETKNSRTRQTVLGLTQTCETLKLQLP 720
QY 721 NCIEDPVSPIVLRNLFSLVGTPLSAFNGLRPLVLAEDAORLFTALFPPEKNCNDNICODD 780
DB 721 NCIEDPVSPIVLRNLFSLVGTPLSAFNGLRPLVLAEDAORLFTALFPPEKNCNDNICODD 780
QY 781 LSITFSFMSLCLVVGGRPFNFVTVVRNDGEDSYRTQVTFPFLDLSYRKVSTLQNRS 840
DB 781 LSITFSFMSLCLVVGGRPFNFVTVVRNDGEDSYRTQVTFPFLDLSYRKVSTLQNRS 840
QY 841 QRSWRLACESASSTEVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLKA 900
DB 841 QRSWRLACESASSTEVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLKA 900
QY 901 NVTSENMPRTNKTEFOLELPVKYAVMVVTSHGVTSTKYLNFNTASENTSRVMOHQYQVSN 960
DB 901 NVTSENMPRTNKTEFOLELPVKYAVMVVTSHGVTSTKYLNFNTASENTSRVMOHQYQVSN 960
QY 961 LGORSLPISLVFLVPLVRLNQTVIWDPRQVTFSENLSSTCHTKERLPSSHDFLAELRKAPV 1020
DB 961 LGORSLPISLVFLVPLVRLNQTVIWDPRQVTFSENLSSTCHTKERLPSSHDFLAELRKAPV 1020
QY 1021 VNCSTANVCORIOCDIPPEGIOEEFNATLKGNSFDWYIKTSHNHLIIVSTAEILLPNDVSF 1080
DB 1021 VNCSTANVCORIOCDIPPEGIOEEFNATLKGNSFDWYIKTSHNHLIIVSTAEILLPNDVSF 1080
QY 1081 TLLPGGAFVRSOTETKVEFPFVNPDLPLIVGSSVGGILLALLIITAAALYKLGFFKQYKD 1140
DB 1081 TLLPGGAFVRSOTETKVEFPFVNPDLPLIVGSSVGGILLALLIITAAALYKLGFFKQYKD 1140
QY 1141 MMSEGGPPGAEPQ 1153
DB 1141 MMSEGGPPGAEPQ 1153

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QY 61 GSYLQCDYSTGCEPIRLQVPVEAVNMSLGLSLAATTSPQLLACGPTVHQTCSNTYVK 120
Db 61 GSYLQCDYSTGCEPIRLQVPVEAVNMSLGLSLAATTSPQLLACGPTVHQTCSNTYVK 120
QY 121 GICFLFSGNLROQPKFPFALRGCPQEDSDIAFLIDGSGIIPHFRMKKEVSTVMEQL 180
Db 121 GICFLFSGNLROQPKFPFALRGCPQEDSDIAFLIDGSGIIPHFRMKKEVSTVMEQL 180
QY 181 KKSCTLFLSMQYSEBFRIHFTFKFQNNPNPSLVKPIQLLGRTHATGIRKVVRELFN 240
Db 181 KKSCTLFLSMQYSEBFRIHFTFKFQNNPNPSLVKPIQLLGRTHATGIRKVVRELFN 240
QY 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVPIPEADREGVIRYVIGVDAPFSEKSRQEL 300
Db 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVPIPEADREGVIRYVIGVDAPFSEKSRQEL 300
QY 301 NTIASKPPRDHVQVNNFEALKTIONLREKFALEGOTGSSSFEHMSQEGFSAAIT 360
Db 301 NTIASKPPRDHVQVNNFEALKTIONLREKFALEGOTGSSSFEHMSQEGFSAAIT 360
QY 361 SNGPLLLSTVGSYDAGGVFLYTSKEKSTFINNTRVDSMDNDAYLGYAAAIILRNVRQSLV 420
Db 361 SNGPLLLSTVGSYDAGGVFLYTSKEKSTFINNTRVDSMDNDAYLGYAAAIILRNVRQSLV 420
QY 421 LGAPRYQHIGLVAMFRONTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLLVIGAP 480
Db 421 LGAPRYQHIGLVAMFRONTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLLVIGAP 480
QY 481 HYYETRGQGVSVCPPLPRGORARWOCDAVLGYEQQOPWGRFGAALTVLGDVNGDKLTDVA 540
Db 481 HYYETRGQGVSVCPPLPRGORARWOCDAVLGYEQQOPWGRFGAALTVLGDVNGDKLTDVA 540
QY 541 IGAPCEEDNRGAVILFHGTSGSGISPHSQRTAGSKLSPRLQYFGQSLSGGQDLTMDGLV 600
Db 541 IGAPCEEDNRGAVILFHGTSGSGISPHSQRTAGSKLSPRLQYFGQSLSGGQDLTMDGLV 600
QY 601 DLTVGAQGHVLLRSQPVLRVKAIMEFNPREVARNVFECDQVVKGEAGEVRVCLHVQK 660
Db 601 DLTVGAQGHVLLRSQPVLRVKAIMEFNPREVARNVFECDQVVKGEAGEVRVCLHVQK 660
QY 661 STRDLRREGIOISVVTYDIALDSGRPHSAVNENKSTRROTQVLGLTOTCETLKLQIP 720
Db 661 STRDLRREGIOISVVTYDIALDSGRPHSAVNENKSTRROTQVLGLTOTCETLKLQIP 720
QY 721 NCIEDPVSPIVLRNPLSLVGTPLSAFGLNRPVLAEDAQLFTALPPFEKNCNDNIQDD 780
Db 721 NCIEDPVSPIVLRNPLSLVGTPLSAFGLNRPVLAEDAQLFTALPPFEKNCNDNIQDD 780
QY 781 LSITFSFMSLDCLVVGGPREFNTVTRNDGSDSYRTQVTFPPFLDLSYRKVSTLQNRS 840
Db 781 LSITFSFMSLDCLVVGGPREFNTVTRNDGSDSYRTQVTFPPFLDLSYRKVSTLQNRS 840
QY 841 QRSWLACESASSTEVSGALKSTCSINHPPIPENSEVTFNITFDVDSKASLGNKLLKA 900
Db 841 QRSWLACESASSTEVSGALKSTCSINHPPIPENSEVTFNITFDVDSKASLGNKLLKA 900
QY 901 NVTSENMPRTNKTPEQLPVLKYAVYVMTVSHGVSTKYNLTASNTRSVNMQHOVQSN 960
Db 901 NVTSENMPRTNKTPEQLPVLKYAVYVMTVSHGVSTKYNLTASNTRSVNMQHOVQSN 960
QY 961 LGQRLSPLSLVLPVRLNQTVWDRPQVTFSENLSSTCHTKERLPSSHDFLAEIRKAPV 1020
Db 961 LGQRLSPLSLVLPVRLNQTVWDRPQVTFSENLSSTCHTKERLPSSHDFLAEIRKAPV 1020
QY 1021 VNCSTAVCQRIQCDIPFFGIQEEFNATLKGNSFDWYIKTSHNHLIIVSTABILFNDSVF 1080
Db 1021 VNCSTAVCQRIQCDIPFFGIQEEFNATLKGNSFDWYIKTSHNHLIIVSTABILFNDSVF 1080
QY 1081 TLLPGQCAFVRSQTEFKVBPFPVNPPLIIVGSSVGGILLALLITAALYKLGFFFKQYKD 1140
Db 1081 TLLPGQCAFVRSQTEFKVBPFPVNPPLIIVGSSVGGILLALLITAALYKLGFFFKQYKD 1140
QY 1141 MMSEGGPPGAEPQ 1153
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Db 1141 MMSEGGPPGAEPQ 1153
RESULT 6
US-09-945-265-4
; Sequence 4, Application US/09945265
; Patent No. US20020123614A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy A.
; APPLICANT: Shimaoka, Motomu
; APPLICANT: Lu, Chafen
; TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A
; FILE REFERENCE: CBN-002CP
; CURRENT APPLICATION NUMBER: US/09/945,265
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,700
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-945-265-4
Query Match 99.7%; Score 5937.5; DB 9; Length 1152;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1151; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
QY 1 MALRVLLLTALTLCGCFNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIIVAANQR 60
Db 1 MALRVLLLTALTLCGCFNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIIVAANQR 60
QY 61 GSYLQCDYSTGCEPIRLQVPVEAVNMSLGLSLAATTSPQLLACGPTVHQTCSNTYVK 120
Db 61 GSYLQCDYSTGCEPIRLQVPVEAVNMSLGLSLAATTSPQLLACGPTVHQTCSNTYVK 120
QY 121 GICFLFSGNLROQPKFPFALRGCPQEDSDIAFLIDGSGIIPHFRMKKEVSTVMEQL 180
Db 121 GICFLFSGNLROQPKFPFALRGCPQEDSDIAFLIDGSGIIPHFRMKKEVSTVMEQL 180
QY 181 KKSCTLFLSMQYSEBFRIHFTFKFQNNPNPSLVKPIQLLGRTHATGIRKVVRELFN 240
Db 181 KKSCTLFLSMQYSEBFRIHFTFKFQNNPNPSLVKPIQLLGRTHATGIRKVVRELFN 240
QY 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVPIPEADREGVIRYVIGVDAPFSEKSRQEL 300
Db 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVPIPEADREGVIRYVIGVDAPFSEKSRQEL 300
QY 301 NTIASKPPRDHVQVNNFEALKTIONLREKFALEGOTGSSSFEHMSQEGFSAAIT 360
Db 301 NTIASKPPRDHVQVNNFEALKTIONLREKFALEGOTGSSSFEHMSQEGFSAAIT 360
QY 361 SNGPLLLSTVGSYDAGGVFLYTSKEKSTFINNTRVDSMDNDAYLGYAAAIILRNVRQSLV 420
Db 361 SNGPLLLSTVGSYDAGGVFLYTSKEKSTFINNTRVDSMDNDAYLGYAAAIILRNVRQSLV 420
QY 421 LGAPRYQHIGLVAMFRONTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLLVIGAP 480
Db 421 LGAPRYQHIGLVAMFRONTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLLVIGAP 480
QY 481 HYYETRGQGVSVCPPLPRGORARWOCDAVLGYEQQOPWGRFGAALTVLGDVNGDKLTDVA 540
Db 481 HYYETRGQGVSVCPPLPRGORARWOCDAVLGYEQQOPWGRFGAALTVLGDVNGDKLTDVA 540
QY 541 IGAPCEEDNRGAVILFHGTSGSGISPHSQRTAGSKLSPRLQYFGQSLSGGQDLTMDGLV 600
Db 540 IGAPCEEDNRGAVILFHGTSGSGISPHSQRTAGSKLSPRLQYFGQSLSGGQDLTMDGLV 599
QY 601 DLTVGAQGHVLLRSQPVLRVKAIMEFNPREVARNVFECDQVVKGEAGEVRVCLHVQK 660
Db 601 DLTVGAQGHVLLRSQPVLRVKAIMEFNPREVARNVFECDQVVKGEAGEVRVCLHVQK 660
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Db 600 DLTVGAQGHVLLRSQVLRVKAIMEFNPREVARNVFECDNDQVVGKEAGEVRVCLHVQK 659
QY 661 STRDLREGQIQSVVTVYDLALDSGRPHSRVAFNETKNSRTRQVGLTQTCETLKLQLP 720
Db 660 STRDLREGQIQSVVTVYDLALDSGRPHSRVAFNETKNSRTRQVGLTQTCETLKLQLP 719
QY 721 NCIEDPVSPIVLRNLSFVLTPLSAFGLNRPVLAEDAQRLLFTALFFPEKNCNDNIQQDD 780
Db 720 NCIEDPVSPIVLRNLSFVLTPLSAFGLNRPVLAEDAQRLLFTALFFPEKNCNDNIQQDD 779
QY 781 LSITFSFMSDCLVVGPRBNVTVVRNDGDSYRTQVTFPPPLDLSYRKVSTLQNR 840
Db 780 LSITFSFMSDCLVVGPRBNVTVVRNDGDSYRTQVTFPPPLDLSYRKVSTLQNR 839
QY 841 QRSWRLACESASSTVSGALKSTSCSINHPIFPENSEVTNITFDVDSKASLGKLLIKA 900
Db 840 QRSWRLACESASSTVSGALKSTSCSINHPIFPENSEVTNITFDVDSKASLGKLLIKA 899
QY 901 NVTSNNMPTNKTETQLELPVKYAVVMVTVSHGVSTKYNFTASNTSRVMQHOVQSN 960
Db 900 NVTSNNMPTNKTETQLELPVKYAVVMVTVSHGVSTKYNFTASNTSRVMQHOVQSN 959
QY 961 LGORSLSPIVLRNLSFVLTPLSAFGLNRPVLAEDAQRLLFTALFFPEKNCNDNIQQDD 1020
Db 960 LGORSLSPIVLRNLSFVLTPLSAFGLNRPVLAEDAQRLLFTALFFPEKNCNDNIQQDD 1019
QY 1021 VNCISIAVCORIQQDIPFFGQIEEFNATLKGNSLFDWYIKTSHNHLIIVSTAELFNDSVF 1080
Db 1020 VNCISIAVCORIQQDIPFFGQIEEFNATLKGNSLFDWYIKTSHNHLIIVSTAELFNDSVF 1079
QY 1081 TLLPGQCAFVRSQTEKVPFFVNPPLIIVGSSVGLLALLIITAALYKLGFFKRYQKD 1140
Db 1080 TLLPGQCAFVRSQTEKVPFFVNPPLIIVGSSVGLLALLIITAALYKLGFFKRYQKD 1139
QY 1141 MNSEGPPGAEQ 1153
Db 1140 MNSEGPPGAEQ 1152

RESULT 7
US-09-902-481A-6
; Sequence 6, Application US/09902481A
; Publication No. US20030054440A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy
; APPLICANT: Shimooka, Motomu
; APPLICANT: Shifman, Julia
; APPLICANT: Mayo, Stephen
; TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
; FILE REFERENCE: A-70586-1/RPT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/902,481A
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/216,600
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 1137
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-902-481A-6

Query Match 98.5%; Score 5865; DB 10; Length 1137;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1132; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 17 ENLDTENAMTQENARGQSVVQLQGRVVVVGAPQEIIVAAQRGSLYQCDYSTGSCPEI 76
Db 1 ENLDTENAMTQENARGQSVVQLQGRVVVVGAPQEIIVAAQRGSLYQCDYSTGSCPEI 60
QY 77 RLQVPVEAVNMSLGLSLAATTSPQLLACGPTVHTQCSNTYVKGCLFLGSLNRQQPQK 136

US-09-902-481A-5
; Sequence 5, Application US/09902481A
; Publication No. US2003005440A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy
; APPLICANT: Shimaoka, Motomu
; APPLICANT: Shifman, Julia
; APPLICANT: Mayo, Stephen
; TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
; FILE REFERENCE: A-70586-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/902,481A
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/216,600
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1137
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-902-481A-5
Query Match 98.4%; Score 5859; DB 10; Length 1137;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1128; Conservative 8; Mismatches 1; Indels 0; Gaps 0;
QY 17 FNLDTENAMTFQENARGFGQSVVQLQGSRRVVVGAPQEIIVAANQKSLYQCDYSTGSCBPI 76
DB 1 FNLDTENAMTFQENARGFGQSVVQLQGSRRVVVGAPQEIIVAANQKSLYQCDYSTGSCBPI 60
QY 77 RLQVPVEAVNMSLGLSLAATTSPPQLLAGCGTTHQTCSEYTYVKGCLFGLFNSLRQKQK 136
DB 61 RLQVPVEAVNMSLGLSLAATTSPPQLLAGCGTTHQTCSEYTYVKGCLFGLFNSLRQKQK 120
QY 137 PPEALRGCPQSDSDIAFLIDGSGSIIPHDPRFMKEFVSTVMBQKSKTFLSLMOYSBEF 196
DB 121 PPEALRGCPQSDSDIAFLIDGSGSIIPHDPRFRAKEFISTVMBQKSKTFLSLMOYSBEF 180
QY 197 RIHFTFKFQNNPNSRLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVI 256
DB 181 RIHFTFKFQNNPNSRLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVI 240
QY 257 TDGEKFGDPLGYEDVPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPDRHVFQV 316
DB 241 TDGEKFGDPLGYEDVPEADREGVIRYVIGVGDAFRSEKSRQELNTVASKPPDRHVFQIN 300
QY 317 NPEALKTIQNLQREKFAIEGTQTSSESSFEHMSQEGFSAAITNSGPLLSTVGSDYDAG 376
DB 301 NPEALKTIQNLQREKFAIEGTQTSSESSFEHMSQEGFSAAITNSGPLLSTVGSDYDAG 360
QY 377 GVFLYTSKEKSTFINMTRVDSMDNDAYLGAAATILRNVRQSLVLGAPRYQHIGLVAMFR 436
DB 361 GVFLYTSKEKSTFINMTRVDSMDNDAYLGAAATILRNVRQSLVLGAPRYQHIGLVAMFR 420
QY 437 QNTGWESNANVKGITQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQSVSCPL 496
DB 421 QNTGWESNANVKGITQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQSVSCPL 480
QY 497 PRGQARWQCDVAVLGEQGPWGRFGAALTVDGVNGDKLTDVAICAPGEEDNRGANVLF 556
DB 481 PRGQARWQCDVAVLGEQGPWGRFGAALTVDGVNGDKLTDVAICAPGEEDNRGANVLF 540
QY 557 HGTSGSGISPSHSORIAKSLPRLOYFGOSLGGQDLTMDGLVDLTVCAGQSHVLLRSQ 616
DB 541 HGTSGSGISPSHSORIAKSLPRLOYFGOSLGGQDLTMDGLVDLTVCAGQSHVLLRSQ 600
QY 617 PVLVRKAIEMFNPREVARNVFCNDQVWKGKAGEVRVCLHVQKSTRDLREGQIQSVVT 676
DB 601 PVLVRKAIEMFNPREVARNVFCNDQVWKGKAGEVRVCLHVQKSTRDLREGQIQSVVT 660
QY 677 YDLALDSGRPHSRVFNFTKSTRQTQVLGTLQTCETLKLQPLNCIEDPVSPIVLRNF 736

DB 661 YDLALDSGRPHSRVFNFTKSTRQTQVLGTLQTCETLKLQPLNCIEDPVSPIVLRNF 720
QY 737 SLVGTPLSAFGNLRPLVLAEDAQRLLFTALFPPEKKNCGNDNI CODDLSITFSFMSLDCLVVG 796
DB 721 SLVGTPLSAFGNLRPLVLAEDAQRLLFTALFPPEKKNCGNDNI CODDLSITFSFMSLDCLVVG 780
QY 797 GPREFNVTVVRNDGEDSYRTQVTFPPFLDLSYRKVSTLQNRQSRWRLACESASSTEV 856
DB 781 GPREFNVTVVRNDGEDSYRTQVTFPPFLDLSYRKVSTLQNRQSRWRLACESASSTEV 840
QY 857 SGALKSTSCSINHPIFPENSEVTENITFDVSKASLGNKLLKANVTSENNMPTNKTEF 916
DB 841 SGALKSTSCSINHPIFPENSEVTENITFDVSKASLGNKLLKANVTSENNMPTNKTEF 900
QY 917 QLELPVKYAVVMVVTSHGVSTKYLNFNTASENTSRVMQHQYQVSNLQKSLPLSLVFLVPV 976
DB 901 QLELPVKYAVVMVVTSHGVSTKYLNFNTASENTSRVMQHQYQVSNLQKSLPLSLVFLVPV 960
QY 977 RLNQTVIWDPRQVTFSENLSTCHTKERLPSHSDPLAELRKAPVNVNCISIAVCQRIQCDIP 1036
DB 961 RLNQTVIWDPRQVTFSENLSTCHTKERLPSHSDPLAELRKAPVNVNCISIAVCQRIQCDIP 1020
QY 1037 PFGIOEEFNATLKGNSLSDWYIKTSHNHLIIVSTAEILFNDVSFTLLPQCGAFVRSOTET 1096
DB 1021 PFGIOEEFNATLKGNSLSDWYIKTSHNHLIIVSTAEILFNDVSFTLLPQCGAFVRSOTET 1080
QY 1097 KVEPPEVENPLPLIVGSSVGGLLIALLITAAALYKLGFFKQYKDMMSGGPPGABPQ 1153
DB 1081 KVEPPEVENPLPLIVGSSVGGLLIALLITAAALYKLGFFKQYKDMMSGGPPGABPQ 1137
RESULT 9
US-09-902-481A-4
; Sequence 4, Application US/09902481A
; Publication No. US2003005440A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy
; APPLICANT: Shimaoka, Motomu
; APPLICANT: Shifman, Julia
; APPLICANT: Mayo, Stephen
; TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
; FILE REFERENCE: A-70586-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/902,481A
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/216,600
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1137
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-902-481A-4
Query Match 98.3%; Score 5849; DB 10; Length 1137;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1127; Conservative 8; Mismatches 2; Indels 0; Gaps 0;
QY 17 FNLDTENAMTFQENARGFGQSVVQLQGSRRVVVGAPQEIIVAANQKSLYQCDYSTGSCBPI 76
DB 1 FNLDTENAMTFQENARGFGQSVVQLQGSRRVVVGAPQEIIVAANQKSLYQCDYSTGSCBPI 60
QY 77 RLQVPVEAVNMSLGLSLAATTSPPQLLAGCGTTHQTCSEYTYVKGCLFGLFNSLRQKQK 136
DB 61 RLQVPVEAVNMSLGLSLAATTSPPQLLAGCGTTHQTCSEYTYVKGCLFGLFNSLRQKQK 120
QY 137 PPEALRGCPQSDSDIAFLIDGSGSIIPHDPRFMKEFVSTVMBQKSKTFLSLMOYSBEF 196
DB 121 PPEALRGCPQSDSDIAFLIDGSGSIIPHDPRFMKEFVSTVMBQKSKTFLSLMOYSBEF 180

QY 197 RIHFTKEFQNNPNRSLVKPTQLLGRTHHTATGIRKVVRELFNITNGARKNAFKILVVI 256
DB 181 RIHFTKEFQNNPNRSLVKPTQLLGRTHHTATGIRKVVRELFNITNGARKNAFKILFLL 240
QY 257 TDGEKFGDPLGYEDVTPEDRGGVRYVIGVDGAPRSEKSRQELANTIASKPPDRDHVQVN 316
DB 241 TDGEKFGDPLGYEDVTPEDRGGVRYVIGVDGAPRSEKSRQELANTIASKPPDRDHVQVN 300
QY 317 NFEALKTIONLREKXFAIEGTQTGSSSFEHMSQEGFSAAITNGPLLSITVGSYDNAG 376
DB 301 NFEALKTIONLREKXFAIEGTQTGSSSFEHMSQEGFSAAITNGPLLSITVGSYDNAG 360
QY 377 GVFLYTSKESKSTFINMTRVDSMDNDAYLGAAAILRNVRQSLVIGAPRYOHIGLVAMFR 436
DB 361 GVFLYTSKESKSTFINMTRVDSMDNDAYLGAAAILRNVRQSLVIGAPRYOHIGLVAMFR 420
QY 437 QNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDVLIGAPHYVETRGQVSVCP 496
DB 421 QNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDVLIGAPHYVETRGQVSVCP 480
QY 497 PRGQARWQCDVAVLYGEGQGPWRFGAALTVDVGVNGDKLTDVAIGAPGEEDNRGAVYLF 556
DB 481 PRGQARWQCDVAVLYGEGQGPWRFGAALTVDVGVNGDKLTDVAIGAPGEEDNRGAVYLF 540
QY 557 HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTGVAQGHVLLRSQ 616
DB 541 HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTGVAQGHVLLRSQ 600
QY 617 PVLRVKAIMFNPREVARNVPECNDQVVKGEAGEVRVCLHVOKSTRDLREGQIQSVVT 676
DB 601 PVLRVKAIMFNPREVARNVPECNDQVVKGEAGEVRVCLHVOKSTRDLREGQIQSVVT 660
QY 677 YDLALDSGRPHSRAVFNETKNSTRQTQVLGTLQTCETLKLQPLNCIEDPVSPIVLRNF 736
DB 661 YDLALDSGRPHSRAVFNETKNSTRQTQVLGTLQTCETLKLQPLNCIEDPVSPIVLRNF 720
QY 737 SLVGTPLSAFNGLRPVLAEADAQRLLFTALFPFEKNCNDNI CODDLSITFSFMSLDCLVVG 796
DB 721 SLVGTPLSAFNGLRPVLAEADAQRLLFTALFPFEKNCNDNI CODDLSITFSFMSLDCLVVG 780
QY 797 GPRENVTVTVNDGEDSVRTQVTFPPDLDSYRKVSTLQORSORSWRLACESASSTEV 856
DB 781 GPRENVTVTVNDGEDSVRTQVTFPPDLDSYRKVSTLQORSORSWRLACESASSTEV 840
QY 857 SGALKSTCSINHPIFPENSEVTENITFDVDSKASLGNKLLKANVTSENNMPRTNTEF 916
DB 841 SGALKSTCSINHPIFPENSEVTENITFDVDSKASLGNKLLKANVTSENNMPRTNTEF 900
QY 917 QLELPVKYAVVMVTSHGVS TKYLNFTASENTRVMOHQYQVSNLQORSLSPISLVFLVPV 976
DB 901 QLELPVKYAVVMVTSHGVS TKYLNFTASENTRVMOHQYQVSNLQORSLSPISLVFLVPV 960
QY 977 RLNQTVIWDROPVTFSENLSSCTCHTKERLPHSDDFLAELKAPVVCNSIACQRTQCDIP 1036
DB 961 RLNQTVIWDROPVTFSENLSSCTCHTKERLPHSDDFLAELKAPVVCNSIACQRTQCDIP 1020
QY 1037 PFGIQEEFNATLKGNSLFDWIKTSHNHLIVSTAEILFNDSVFTLLPQCGAFVRSQTE 1096
DB 1021 PFGIQEEFNATLKGNSLFDWIKTSHNHLIVSTAEILFNDSVFTLLPQCGAFVRSQTE 1080
QY 1097 KVEPEVNPPLIIVGSSVGLLILALITAAALYKLGPFKQYKQKMSGGPPGABPQ 1153
DB 1081 KVEPEVNPPLIIVGSSVGLLILALITAAALYKLGPFKQYKQKMSGGPPGABPQ 1137

RESULT 10

US-09-902-481A-3
; Sequence 3, Application US/09902481A
; Publication No. US2003005440A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy
; APPLICANT: Shimaoka, Motomu
; APPLICANT: Shifman, Julia

; APPLICANT: Mayo, Stephen
; TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
; FILE REFERENCE: A-70586-1/RPT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/902,481A
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/216,600
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1137
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-902-481A-3

Query Match 98.0%; Score 5836; DB 10; Length 1137;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1123; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 17 ENLDTENAMTFOENARGFGOSVVOLOQSRVVVGAPQETVAANORGSLYQCDYSTGSCPEI 76
DB 1 ENLDTENAMTFOENARGFGOSVVOLOQSRVVVGAPQETVAANORGSLYQCDYSTGSCPEI 60
QY 77 RLQVPVEAVNMVSLGLSLAAATSPPLLACGPTVHTQTCSENYVVGKLCFLFGSNLRQPOK 136
DB 61 RLQVPVEAVNMVSLGLSLAAATSPPLLACGPTVHTQTCSENYVVGKLCFLFGSNLRQPOK 120
QY 137 PPEALRGCPQSDSDIAFLIDGSGSIIIPDFFRMKEFVSTVMEQKKSKTLPSLMQYSEEP 196
DB 121 PPEALRGCPQSDSDIAFLIDGSGSIIIPDFFRMKEFVSTVMEQKKSKTLPSLMQYSEEP 180
QY 197 RIHTEKEFQNNPNRSLVKPTQLLGRTHHTATGIRKVVRELFNITNGARKNAFKILVVI 256
DB 181 RIHTEKEFQNNPNRSLVKPTQLLGRTHHTATGIRKVVRELFNITNGARKNAFKILFLL 240
QY 257 TDGEKFGDPLGYEDVTPEDRGGVRYVIGVDGAPRSEKSRQELNTIASKPPDRDHVQVN 316
DB 241 TDGEKFGDPLGYEDVTPEDRGGVRYVIGVDGAPRSEKSRQELNTIASKPPDRDHVQVN 300
QY 317 NFEALKTIONLREKXFAIEGTQTGSSSFEHMSQEGFSAAITNGPLLSITVGSYDNAG 376
DB 301 NFEALKTIONLREKXFAIEGTQTGSSSFEHMSQEGFSAAITNGPLLSITVGSYDNAG 360
QY 377 GVFLYTSKESKSTFINMTRVDSMDNDAYLGAAAILRNVRQSLVIGAPRYOHIGLVAMFR 436
DB 361 GVFLYTSKESKSTFINMTRVDSMDNDAYLGAAAILRNVRQSLVIGAPRYOHIGLVAMFR 420
QY 437 QNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDVLIGAPHYVETRGQVSVCP 496
DB 421 QNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDVLIGAPHYVETRGQVSVCP 480
QY 497 PRGQARWQCDVAVLYGEGQGPWRFGAALTVDVGVNGDKLTDVAIGAPGEEDNRGAVYLF 556
DB 481 PRGQARWQCDVAVLYGEGQGPWRFGAALTVDVGVNGDKLTDVAIGAPGEEDNRGAVYLF 540
QY 557 HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTGVAQGHVLLRSQ 616
DB 541 HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTGVAQGHVLLRSQ 600
QY 617 PVLRVKAIMFNPREVARNVPECNDQVVKGEAGEVRVCLHVOKSTRDLREGQIQSVVT 676
DB 601 PVLRVKAIMFNPREVARNVPECNDQVVKGEAGEVRVCLHVOKSTRDLREGQIQSVVT 660
QY 677 YDLALDSGRPHSRAVFNETKNSTRQTQVLGTLQTCETLKLQPLNCIEDPVSPIVLRNF 736
DB 661 YDLALDSGRPHSRAVFNETKNSTRQTQVLGTLQTCETLKLQPLNCIEDPVSPIVLRNF 720
QY 737 SLVGTPLSAFNGLRPVLAEADAQRLLFTALFPFEKNCNDNI CODDLSITFSFMSLDCLVVG 796
DB 721 SLVGTPLSAFNGLRPVLAEADAQRLLFTALFPFEKNCNDNI CODDLSITFSFMSLDCLVVG 780

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QY 797 GPRENVTVVRNDCGDSYRTQVTFPPFLDLISYRKVSTLQNRORSWRLACESASGEV 856
Db 781 GPRENVTVVRNDCGDSYRTQVTFPPFLDLISYRKVSTLQNRORSWRLACESASGEV 840
QY 857 SGALKSTSCSINHPIPPENSEVTNITFDVDSKASLGNKLLKANVTSENNMPTNKTEP 916
Db 841 SGALKSTSCSINHPIPPENSEVTNITFDVDSKASLGNKLLKANVTSENNMPTNKTEP 900
QY 917 QLELPVKAVYVMVTVSHGVSTKYLNFTASENTRVMQHQYQVSNLQORSLSPLSLVFLVPV 976
Db 901 QLELPVKAVYVMVTVSHGVSTKYLNFTASENTRVMQHQYQVSNLQORSLSPLSLVFLVPV 960
QY 977 RLNQTVIWRDPQVTSSENLSSCTCHTKERLPSHSDFLAELRKAPVVCNCSIAVQRIQCDDIP 1036
Db 961 RLNQTVIWRDPQVTSSENLSSCTCHTKERLPSHSDFLAELRKAPVVCNCSIAVQRIQCDDIP 1020
QY 1037 PFGIOEEFNATLKGNSLFDWYIKTSHNHLIIVSTAEILFNDSVFTLLPQOGAFVRSQTEP 1096
Db 1021 PFGIOEEFNATLKGNSLFDWYIKTSHNHLIIVSTAEILFNDSVFTLLPQOGAFVRSQTEP 1080
QY 1097 KVEPPEVFNPLPLIIVGSSVGGLLALLTAALYKLGFFKQYKQVCOMMSSEGGPPGAEPPQ 1153
Db 1081 KVEPPEVFNPLPLIIVGSSVGGLLALLTAALYKLGFFKQYKQVCOMMSSEGGPPGAEPPQ 1137

RESULT 11
US-10-116-275-204
; Sequence 204, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; FILE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
; FILE REFERENCE: E1067/20087
; CURRENT APPLICATION NUMBER: US/10/116,275
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 204
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-275-204

Query Match 58.8%; Score 3500; DB 14; Length 1163;
Best Local Similarity 61.3%; Pred. No. 6.8e-280;
Matches 699; Conservative 139; Mismatches 297; Indels 6; Gaps 4;

QY 5 VLLLTALTLCHFNLDNTENMTFOENARGFGOSVVLQGRVVGACQEIIVANQORSIJ 64
Db 8 LLLFTALATSLGFLNLDTELTAFRDYAGFGDSVQYANVWVGAPQKITAANQTGLY 67
QY 65 QCDYGTGSCPTRLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSNTYVKGLCF 124
Db 68 QCGYSTGACEPIGLQVPEAVNMSLGLSLASTTSQQLACGPTVHCEGRNMYITGLCF 127
QY 125 LFGSNLRQOPKFPBALRGCPQEDSDIAPLDGSGSIIPHPDPRMKEFVSTVMEQLKXSK 184
Db 128 LLGPT--QUTRLPVSRQBCPQEQDIFVLIDGSGSISRNPNATMNFVRAVISQFQRP 185
QY 185 TLPSLMQVSEERIHFTFEKQPNPNRSLVXPITQLGRTHATGIRKVVRELNIYNG 244
Db 186 TOFSLMQFSNKQTHTFEFPRRTNPLSLASVHQLQGTFTYTAIONVHRLPHASYG 245
QY 245 ARKNAPKILWITDGEKFDGLGYDVIPEADREGVIRVIGVDAFRSEKRSQELNTIA 304
Db 246 ARDATKILIVITDGKSGDSLQKDVIPMADAAGIIRYAIUGLAFQNRNSWKLNDIA 305
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QY 305 SKPRDHHVQVNNFEALKTIONQREKXFALEGTOQTSSSSFEHEMSQEGSAAITSNGP 364
Db 306 SKPSQEHIFKVEDFDALKDIONQLKEKIFALEGTETTSSSSFELEMAQEGSAVPTDGP 365
QY 365 LLSTVGSVDWAGGVPLATSKSEKSTFINWTRVDSNDWDAYLVAAAIILRNVRQSLVIGAP 424
Db 366 VLGAVGFTWGGAPLTPPNMSPPTFINNSQENVMRDSYLGISTELALWKGVQSLVIGAP 425
QY 425 RYOHIGLVAMFRQNTGMWESNANYKGTQIGAYFGASLCSVDVDSNGSTDLDLIGAPHYYE 484
Db 426 RYQHTGRAVITQVSRQWRMKAETVGTQIGSYFGASLCSVDVDTDGSDDLVLIGAPHYYE 485
QY 485 QTRGGQVSVCLPRGQARWOCDAVLGEGQQQWGRFGAALTIVLGDVNGDKLTVDAIGAP 544
Db 486 QTRGGQVSVCLPRGWR--RWCMDAVLYGEGQHPGRFGAALTIVLGDVNGDKLTVDAIGAP 544
QY 545 GEENRGAVLYFCHTSGSGISPSHQSORTAGSKLSPRLQYFGQSLSGGODLMDGLVDLTV 604
Db 545 GEENRGAVLYFCHTSGSGISPSHQSORTAGSKLSPRLQYFGQSLSGGODLMDGLVDLTV 604
QY 605 GAQGHVLLLRSPQVLRVKAIMFNPREVARNVFECNDQVVKGEAGEVRVCLHVKQSTRD 664
Db 605 GARGOVLLLRTPVLWVGVSQMFIPAEIPRSAFECEQVWSEQTLVQSNICLIYDKRSKN 664
QY 724 RLREGQIQSVTVYDLALDSGRPHSAVNETKNSRTRQTVGLGTQTCETLKLQPNCLIE 724
Db 665 LLGRDLQSSVTLDLALDPGRLLSPRATPQETKNSRSLSRVRLGLKAHCENFLLPSCVE 724
QY 725 DPVSPVILRLNFSLVGTPLSAFAGNLRPVLAEDADRLFTALPFEKNCNDNINCOODLSIT 784
Db 725 DSVTPITLRLNFTLVGKPLLAFLRMLRPMALAAQRYFTASLPFEKNCADHICQDNLGIS 784
QY 785 FSPMSLDCLVVGGPREFNVTYVRNDCGDSYRTQVTFPPFLDLISYRKVSTLQNRORSW 844
Db 785 FSPFGLKSLVGSNLENAEVMVWVNDGDSYGTITTFSPAGLSYRYVAEGQKQGLRSL 844
QY 845 RLACESASTSEVGALKSTSCSINHPIPPENSEVTNITFDVDSKASLGNKLLKANVTIS 904
Db 845 HLTCDSPVPG--SQGTWSTSCRIINHLIFRGGQITFLATFDVSPKAVLGDRLLLTANVSS 902
QY 905 ENNMPTNKTBFQLELPVKYAVYVMVTVSHGVSTKYLNFTAS--ENTSRVMOHQYQVSNLQ 963
Db 903 ENNTPRTSKTTFQLELPVKYAVYVMVTVSHGVSTKYLNFTAS--ENTSRVMOHQYQVSNLQ 962
QY 964 RSLPISLVFLVPLRINQTVIWRDPQVTSSENLSSCTCHTKERLPSHSDFLAELRKAPVVCN 1023
Db 963 RDLPVSNFVWPVELNQEAQVMDVEVSHPPQNSLRCSEKSIAPPASDFLAHQKNPVLDC 1022
QY 1024 SIACVQRIQCDDIPFPGIOEEFNATLKGNSLFDWYIKTSHNHLIIVSTAEILFNDSVFTLL 1083
Db 1023 SIAGCLFRCDVPVSFVQEEELDTLKGNSLFGWVRQILQKVKVSVVSAEITFDTSVYSQ 1082
QY 1084 PQOGAFVRSQTEKVEPEVFNPLPLIIVGSSVGGLLALLTAALYKLGFFKQYKQVCOMMS 1143
Db 1083 PQOGAFVRSQTEKVEPEVFNPLPLIIVGSSVGGLLALLTAALYKLGFFKQYKQVCOMMS 1142
QY 1144 E 1144
Db 1143 E 1143

RESULT 12
US-10-723-860-327
; Sequence 327, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NFUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
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; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 327
; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-327

Query Match      58.8%; Score 3500; DB 17; Length 1163;
Best Local Similarity 61.3%; Pred. No. 6.8e-280;
Matches 699; Conservative 139; Mismatches 297; Indels 6; Gaps 4;

QY 5 VLLLTALTLCHGFLNDTENAMTFQENARGFGQSVVQLOGSRVVVGAPQEIIVAAHQSGSLY 64
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 8 LLLFTALATSLGFLNDTELTAFRVDAGFQSVVQYANSWVVGAPQKITAAQNTGGLY 67
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 65 QCDYSTGSCPIRLQVPVEAVNMSLGLSLAATTSPPQLIACGPTVHQTCSNTYVKGCLCF 124
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 68 QCGYSTGACEPIGLQVPPEAVNMSLGLSLASTTSFQLACGPTVHBCGRNMYLTGLCF 127
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 125 LFGSNLRQOPQKPFPEALRGCPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEOLKSK 184
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 128 LLGPT--QLTORLPVSRQECRQEQDIVFLIDGSGSISRNFATMNFVRAVISQFQPS 185
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 185 TFLSLMOYSEEFRIHFTFKFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNG 244
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 186 TQFSLMQFSNKQTHFTFEEFRRTNPNLSLASVHQLQGGFTTATAIQNVHRLPHASGY 245
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 245 ARKNAFKILVITDGEKFGDPLGYEDVPEADREGVIRYVIGVDGDAFRSEKSRQELNTIA 304
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 246 ARRDATKILVITDGKKEGSDLDYKDVPMDAAGIIRYAGVGLAFQNRNSWKELNDIA 305
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 305 SKPPRDHVPQVNNFALKTIQNLREKPAIAGTQGTGSSSSFEHEMSQEGFSAATISKGP 364
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 306 SKPSQEHIPKVDFDALKDQNLREKPAIAGTQGTGSSSSFEHEMSQEGFSAVFTPDGP 365
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 365 LLSTVGSVDWAGGVFLYTSKERSKTFNTRVDSMDNDAVLGYAAAIILNRNVSQSLVIGAP 424
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Db 366 VLGVGSGFTWAGCAFLYPPNMGPTFNNSQENVMDRDSYLGYSTELALWGVQSJVLVIGAP 425
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 425 RYOHIGLVAMFRONTGMWESNANVKGTOIGAYFGASLCSDVDSDNGSTDVLVIGAPHYFE 484
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Db 426 RYOHGKAVIFQVSRQWRMKAEVGTQIGSYFGASLCSDVDSDNGSTDVLVIGAPHYFE 485
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QY 485 QTRGGQSVCPILPRQORARWQCDVLYGEOGPWGRFGAALTIVLGDVNGDKLTDVIGAP 544
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 486 QTRGGQSVCPILPRQWR--RWWCDVLYGEOGPWGRFGAALTIVLGDVNGDKLTDVIGAP 544
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 545 GEDNRGAVYLPHTGTSGSGISPSHSORLAGSKLSPRLQVFGQSLGGQDLTMDGLVDLTV 604
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Db 545 GEEENRGAVYLPHTGVLGSPISPSHSORLAGSKLSPRLQVFGQALSGQDLTQDGLVDLAV 604
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 605 GAQGHVLLRSQPLRVLRKAIMFENPREVARNVFECDQVVKGEAGEVRVCLVHVKQSTRD 664
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QY 665 RLAREQIQSVTYDLDLSDGRPHSAVNETKNSRTQTVLGLTQTCETLKLQLPNCIE 724
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QY 725 DPVSVILRLNPLSVGTPLSAFNGRLPVLAEDAORLFTALFPFEKNCNGNDNICDDLSIT 784
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QY 785 F5FM5LDCVLVGGPREFNVTVTRVNDGDSYRTQVTFPPFLDLSYKYSTLTQNRQSRSW 844
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QY 845 RLACESASSTSVGALKSTSCSINHIPIPNSESVTFNITFDVDSKASLGKLLKANVTS 904
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Qy 425 RYQHIGLVAMFRQNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDVLIGAPHYYE 484
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RESULT 14

US-09-891-943-4

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; Sequence 4, Application US/09891943
; Publication No. US20030077278A1
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: NO. US20030077278A1el Human 2
; FILE REFERENCE: 27866/35004
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; CURRENT APPLICATION NUMBER: US/09/891,943
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 09/193,043
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/286,889
; PRIOR FILING DATE: 1994-08-05
; PRIOR APPLICATION NUMBER: 08/362,652
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/943,363
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-891-943-4
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Matches 696; Conservative 145; Mismatches 294; Indels 6; Gaps 4;

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Db 426 RYQHIGKAVIFIQVSRQWRMKAIEVIGTQISYFGASLCSVDVDTGSDTLVIGAPHYYE 485
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2005, 15:07:42 ; Search time 55.4108 Seconds
(without alignments)
1379.959 Million cell updates/sec

Title: RWHULB-A

Perfect score: 5953

Sequence: 1 MALRVLLLTALTLCHGFNLD.....FKRQYKDMSEGGPGAPQ 1153

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents_AA.*
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 - 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
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 - 5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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8	5953	100.0	1153	3	US-09-193-043-3
9	5953	100.0	1153	4	US-09-688-307A-3
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21	3477	58.4	1163	2	US-08-482-293A-4
22	3477	58.4	1163	2	US-08-943-363-4
23	3477	58.4	1163	3	US-09-193-043-4
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37	3436.5	57.7	1161	1	US-08-605-672-99	Sequence 99, Appl
38	3436.5	57.7	1161	2	US-08-482-293A-99	Sequence 99, Appl
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40	3436.5	57.7	1161	3	US-09-193-043-99	Sequence 99, Appl
41	3436.5	57.7	1161	4	US-09-688-307A-99	Sequence 99, Appl
42	3436.5	57.7	1161	4	US-09-350-259-99	Sequence 99, Appl
43	3261	54.8	1161	1	US-08-485-618-53	Sequence 53, Appl
44	3261	54.8	1161	1	US-08-362-652-53	Sequence 53, Appl
45	3261	54.8	1161	2	US-08-605-672-53	Sequence 53, Appl

ALIGNMENTS

RESULT 1

US-08-173-497-3
; Sequence 3, Application US/08173497
; Patent No. 5437958
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W Michael
; APPLICANT: Van Der Vieren, Monica
; TITLE OF INVENTION: No. 5437958el Human 2 Integrin Alpha
; TITLE OF INVENTION: Subunit
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 S. Wacker Drive, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,497
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5437958and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/31363
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1153 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-173-497-3

Query Match 100.0%; Score 5953; DB 1; Length 1153;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 3, Application US/08286889
; Patent No. 5470953
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Mich
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/286,889
; APPLICATION NUMBER: US/08/286,889
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: P38,659
; REFERENCE/DOCKET NUMBER: 27866/32168
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1153 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-286-889-3
Query Match 100.0%; Score 5953; DB 1; Length 1153;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MALRVLLLTALTLCGHNLDTENAMTFQENARGQSVVQLQGSRRVVVGAPQEIIVANQR 60
DB 1 MALRVLLLTALTLCGHNLDTENAMTFQENARGQSVVQLQGSRRVVVGAPQEIIVANQR 60
QY 61 GSYLYCDYSTGSCPIRLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSNTYVK 120
DB 61 GSYLYCDYSTGSCPIRLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSNTYVK 120
QY 121 GLCFLFGSNLRQOQKPFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKFVSTVMEQL 180
DB 121 GLCFLFGSNLRQOQKPFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKFVSTVMEQL 180
QY 181 KSKTILFSLMOYSEEPRIHFTFKFQNNPNPSLVKPIITOLLGRHTHTATGIRKVVRELFN 240
DB 181 KSKTILFSLMOYSEEPRIHFTFKFQNNPNPSLVKPIITOLLGRHTHTATGIRKVVRELFN 240
QY 241 ITNGARKNAFKILVITDGEKGPDLGVEDVPIEADREGVIRVYVGVGDAPFRSEKSRQEL 300
DB 241 ITNGARKNAFKILVITDGEKGPDLGVEDVPIEADREGVIRVYVGVGDAPFRSEKSRQEL 300
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QY 301 NTIASKPPDRHVQVNNFEALKTIONQREKXFAIEGTGTGSSSFEHMSQEGFSAIT 360
Db 301 NTIASKPPDRHVQVNNFEALKTIONQREKXFAIEGTGTGSSSFEHMSQEGFSAIT 360
QY 361 SNGPLSTVGSYDAGGVFLYTSKSKSTFINNTRVDSMDNDAYLGYAAAILRNVRQSLV 420
Db 361 SNGPLSTVGSYDAGGVFLYTSKSKSTFINNTRVDSMDNDAYLGYAAAILRNVRQSLV 420
QY 421 LGAPRYQHIGLVAMFRONTGMWESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLIGAP 480
Db 421 LGAPRYQHIGLVAMFRONTGMWESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLIGAP 480
QY 481 HYTEQTRGQVSVCLPRGQRARWQCDVLYGEOQGPWGRFGAALTVLGDVNGDKLTDVA 540
Db 481 HYTEQTRGQVSVCLPRGQRARWQCDVLYGEOQGPWGRFGAALTVLGDVNGDKLTDVA 540
QY 541 IGAPGEEDNRGAVYLFHGTSGSGISPSHSQRTAGSKLSPRLQYFGQSLGGQDLTMDGLV 600
Db 541 IGAPGEEDNRGAVYLFHGTSGSGISPSHSQRTAGSKLSPRLQYFGQSLGGQDLTMDGLV 600
QY 601 DLTGGAQGHVLLRQPVLRVKAIMEFNPREVARNVFECDQVVKGEAGEVRVCLHVQK 660
Db 601 DLTGGAQGHVLLRQPVLRVKAIMEFNPREVARNVFECDQVVKGEAGEVRVCLHVQK 660
QY 661 STRDLREGQIQSVVYTDALDSGRPHSRVAFNETKNSRRTQVGLTQTCTETLKQLP 720
Db 661 STRDLREGQIQSVVYTDALDSGRPHSRVAFNETKNSRRTQVGLTQTCTETLKQLP 720
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Db 781 LSITFSFMSLDCLVGGPREFNVTVVRNDGDSYRTQVTFPFLDLSYRKVSTIQNORS 840
QY 841 QRSWLACESASSTEVSGALKSTCSINHPIPFENSEVTFNITFDVDSKASLGNKLLKA 900
Db 841 QRSWLACESASSTEVSGALKSTCSINHPIPFENSEVTFNITFDVDSKASLGNKLLKA 900
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Db 1021 VNCSIAVCQRIQCDIPFFGIQEEFNATLKGNSLSPDWYIKTSHNLLIYSTABILFNDVSV 1080
QY 1081 TLLPQGGAFVRSQTEKTEPVPNPPLPLIVGSSVGGLLLLALITAAALYKLGFFFRQYKD 1140
Db 1081 TLLPQGGAFVRSQTEKTEPVPNPPLPLIVGSSVGGLLLLALITAAALYKLGFFFRQYKD 1140
QY 1141 MMSEGGPPGABQ 1153
Db 1141 MMSEGGPPGABQ 1153

RESULT 3

US-08-485-618-3
; Sequence 3, Application US/08485618
; Patent No. 5728533
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-618-3

Query Match 100.0%; Score 5953; DB 1; Length 1153;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MALRVLLLTALTLCCHGNLDTENAMTFQENARGFQGSVVQLOGSRVVVGAPQEIVAANOR 60
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Db 61 GSLYQCDYSTGSCPEIRLQVPVEAVNMSLGLSLAATTSPQLLAGCTVHQTCSNTYVK 120
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Db 181 KSKTFLSLMQYSEBFRIHFTFKFQNNPNRSLVKPITQLIGRTHATGIRKVVRELFN 240
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Db 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVITPEADREGVIRYVIGVDAPFSEKSRQEL 300
QY 301 NTIASKPPDRHVQVNNFEALKTIONQREKXFAIEGTGTGSSSFEHMSQEGFSAIT 360
Db 301 NTIASKPPDRHVQVNNFEALKTIONQREKXFAIEGTGTGSSSFEHMSQEGFSAIT 360
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Db 361 SNGPLSTVGSYDAGGVFLYTSKSKSTFINNTRVDSMDNDAYLGYAAAILRNVRQSLV 420
QY 421 LGAPRYQHIGLVAMFRONTGMWESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLIGAP 480

Db 421 LGAPRYQHIGLVAMFRQNTGWSNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLGAP 480
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Db 481 HYEQTTRGGQSVCPPLRGQARWQCDAVLGEOGQPMGRFGAALTVLGDVNGKLTDTVA 540
Qy 541 IGAPGEEDNRGAVLFGHTSGSGISPSHSQRIAGSKLSPRLOYFGQSLSGGQDLTMDGLV 600
Db 541 IGAPGEEDNRGAVLFGHTSGSGISPSHSQRIAGSKLSPRLOYFGQSLSGGQDLTMDGLV 600
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Db 601 DLTVGAQGHVLLRSQPLRVKAIMFNPREFVARNVFCNDQVVKGEAGEVRVCLHVQK 660
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Db 661 STRDLRGQTSQVVTYDIALDSGRPHSRVAFNETKSTRQTQVGLTQTCETLKQLP 720
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Db 781 LSITFSFMSLDCLVVGGPREFNVTVVRNDGEDSYRTQVTFPPFLDLSYRKVSTLQNR 840
Qy 841 QRSWLACESASTSVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLUKA 900
Db 841 QRSWLACESASTSVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLUKA 900
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Db 901 NVTSENNPRTNKTETFOLELPVKYAVMVVTSHGVTSTKYLNFNTASENTSRVQHQYQVSN 960
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Db 961 LQORSLPISLVLVPRNLQTVWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPV 1020
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Db 1021 VNCSTAVCORICODIPFFGIQEEFNATLGNLSFDWYIKTSHNHLIIVSTAEILFNDSVF 1080
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Db 1081 TLLPGQAFVRQOTETKVEPFPVNPPLPLIVGSSVGGLLALLALITAAALKLGFRRQYKD 1140
Qy 1141 NMSEGGPPGABEQ 1153
Db 1141 NMSEGGPPGABEQ 1153

RESULT 4
US-08-362-652-3
; Sequence 3, Application US/08362652
; Patent No. 5766850
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/362,652
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32391
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1153 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-362-652-3

Query Match 100.0%; Score 5953; DB 1; Length 1153;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MALRVLLLTALTLCGHNLDTENAMTFQENARGQSVVOLQGSRRVVGAPQEIIVANQR 60
Db 1 MALRVLLLTALTLCGHNLDTENAMTFQENARGQSVVOLQGSRRVVGAPQEIIVANQR 60
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Db 61 GSLYQCDYSGSCPIRLQVPVEAVNMSLGLSLAATSPOLLACGTVHTQCSNTYVK 120
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Db 181 KKSXTLSLMQYSEFRIHFTTFEFOQNNPNRSLVKPITQLLGRHTATGIRKVVRELFN 240
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Db 241 ITNGARKNAFKILVITDGEKFGDPLGVEDVIPEADREGVIRYVIGVDAPFRSKSQEL 300
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Db 301 NTIASKPPRDHVQVNNFEALKTIONQREKXFAIEGTQTGSSSSSFHEMSQEGFSAIT 360
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Qy 421 LGAPRYQHIGLVAMFRQNTGWSNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLGAP 480
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Qy 481 HYEQTTRGGQSVCPPLRGQARWQCDAVLGEOGQPMGRFGAALTVLGDVNGKLTDTVA 540
Db 481 HYEQTTRGGQSVCPPLRGQARWQCDAVLGEOGQPMGRFGAALTVLGDVNGKLTDTVA 540
Qy 541 IGAPGEEDNRGAVLFGHTSGSGISPSHSQRIAGSKLSPRLOYFGQSLSGGQDLTMDGLV 600
Db 541 IGAPGEEDNRGAVLFGHTSGSGISPSHSQRIAGSKLSPRLOYFGQSLSGGQDLTMDGLV 600
Qy 601 DLTVGAQGHVLLRSQPLRVKAIMFNPREFVARNVFCNDQVVKGEAGEVRVCLHVQK 660
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Db 601 DLTVGAQGHVLLRSQPLRVKALMEFNPREFVARNVFECDQVVKGEAGEVRVCLHVQK 660
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Db 661 STRDLREGQIQSVVYDIALDSGRPHSRAVFNETKNSRRQTQVLGLTQTCTETKLQLP 720
Qy 721 NCIEDPVSPIVLRNFSLVGTPLSAFGLNRPVLAEDAQRLLFTALPFPEKNCNDNICQDD 780
Db 721 NCIEDPVSPIVLRNFSLVGTPLSAFGLNRPVLAEDAQRLLFTALPFPEKNCNDNICQDD 780
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Db 781 LSITFSFMSLDCLVVGGPREFNVTVVRNDGSDSVRTQVTFPPPLDLSVRKYSTLQNGRS 840
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Db 841 QRSWLACESASSTEVSGALKSTCSINHPIPFENSEVTFNITFDVDSKASLGNKLLKA 900
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Db 901 NVTSENNPRTNKTETFOLELPKYAVYVVTSHGVSTKYLNTASENTSRVNMHQYQVSN 960
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Qy 1081 TLLPQGGAFVRSQTKETKVEPVPNPPLPLIVGSSVGGLLLLALITAAALYKLGFFKRYQND 1140
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Db 1141 MMSEGGPPGABQ 1153

RESULT 5
US-08-605-672-3
; Sequence 3, Application US/08605672
; Patent No. 5817515
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/605,672
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994

; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32684
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1153 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-605-672-3

Query Match 100.0%; Score 5953; DB 2; Length 1153;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALRVLLLTALTLCCHGFNLDTENAMTFQENARGFGQSVVQLQGSVVVVGAPQEIIVAANOR 60
Db 1 MALRVLLLTALTLCCHGFNLDTENAMTFQENARGFGQSVVQLQGSVVVVGAPQEIIVAANOR 60
Qy 61 GSLYQCDYSTGCEPIRLQVPVEAVNMSLGLSLAATTSPQQLACGPTVHQTCSNTYVK 120
Db 61 GSLYQCDYSTGCEPIRLQVPVEAVNMSLGLSLAATTSPQQLACGPTVHQTCSNTYVK 120
Qy 121 GLCFLFGNLRQOQKPFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRMRKEFVSTVMEOL 180
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Qy 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVDAPFSEKSRQEL 300
Db 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVDAPFSEKSRQEL 300
Qy 301 NTIASKPPRDHVQVNNFEALKTQNLQREKXFAIEGTQTGSSSSFEHMSQEGSAAIT 360
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Qy 361 SNGPLLSVGSYDAGGVFLYTSKEKSTFINMTRVDSMDNDAYLGAAAILLRNVQSLV 420
Db 361 SNGPLLSVGSYDAGGVFLYTSKEKSTFINMTRVDSMDNDAYLGAAAILLRNVQSLV 420
Qy 421 LGAPRYQHIGLVAMFRQNTGWNESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLIGAP 480
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Qy 541 IGAPGEEDNRGAVLYFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGDLTMDGLV 600
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Qy 601 DLTVGAQGHVLLRSQPLRVKALMEFNPREFVARNVFECDQVVKGEAGEVRVCLHVQK 660
Db 601 DLTVGAQGHVLLRSQPLRVKALMEFNPREFVARNVFECDQVVKGEAGEVRVCLHVQK 660
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Qy 781 LSITFSMSLDCLVGGPREFNTVTVRNDGEDSYRTQVTFPPFLDLSYRKVSTLQNR 840
Db 781 LSITFSMSLDCLVGGPREFNTVTVRNDGEDSYRTQVTFPPFLDLSYRKVSTLQNR 840
Qy 841 QRSWLACESASSTEVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLKA 900
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Qy 901 NVTSENMPRTNKTEFOLELPVKYAVVMVTSHGVSSTKYLNFTASENTSRVMOHQYQVSN 960
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Qy 961 LQQRSLPISLFLVPLRNLQVINDRPOVTFSENLSSTCHTKERLPSHSDFLAELRKP 1020
Db 961 LQQRSLPISLFLVPLRNLQVINDRPOVTFSENLSSTCHTKERLPSHSDFLAELRKP 1020
Qy 1021 VNCSTAVCQRIQCDIPFFGIQEEFNATLKNLSFDWYIKTSHNHLIIVSTAEIIFNDSVF 1080
Db 1021 VNCSTAVCQRIQCDIPFFGIQEEFNATLKNLSFDWYIKTSHNHLIIVSTAEIIFNDSVF 1080
Qy 1081 TLLPQOGAFVRSQRTKVEPPEVNPPLIIVGSSVGGLLALLITAALYKLGFFKROYKD 1140
Db 1081 TLLPQOGAFVRSQRTKVEPPEVNPPLIIVGSSVGGLLALLITAALYKLGFFKROYKD 1140
Qy 1141 MMSEGGPPGABPQ 1153
Db 1141 MMSEGGPPGABPQ 1153

RESULT 6

US-08-482-293A-3
; Sequence 3, Application US/08482293A
; Patent No. 5831029
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshhall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,293A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32684
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 1153 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-482-293A-3
Query Match 100.0%; Score 5953; DB 2; Length 1153;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAURVLLLTALTITLCHGNLDTENAMTFQENARGFQSVQLOGSRVTVGAPQEIIVANQR 60
Db 1 MAURVLLLTALTITLCHGNLDTENAMTFQENARGFQSVQLOGSRVTVGAPQEIIVANQR 60
Qy 61 GSLVQCDYSGTSCBPIRLQVPVEAVNMSLGLSLAATTPOLLACGTVTQTCSENTYVK 120
Db 61 GSLVQCDYSGTSCBPIRLQVPVEAVNMSLGLSLAATTPOLLACGTVTQTCSENTYVK 120
Qy 121 GLCFLFGSNLRQQPKFPEALRGCPQEDSDIAFLIDGSGSIIIPHDFRMKEFVSTVMEQL 180
Db 121 GLCFLFGSNLRQQPKFPEALRGCPQEDSDIAFLIDGSGSIIIPHDFRMKEFVSTVMEQL 180
Qy 181 KKSXTLFLSMQYSEEFRIHFTFKFQNNPNRSLVKDITQLLGRTHATGIRKVVRELFN 240
Db 181 KKSXTLFLSMQYSEEFRIHFTFKFQNNPNRSLVKDITQLLGRTHATGIRKVVRELFN 240
Qy 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVPEADREGVIRVYVIGVDAPRSEKSRQEL 300
Db 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVPEADREGVIRVYVIGVDAPRSEKSRQEL 300
Qy 301 NTIASKPPDRHVFOVNNFEALKTIONQREKFAIEGTQTGSSSSFEHMSQEGFSAIT 360
Db 301 NTIASKPPDRHVFOVNNFEALKTIONQREKFAIEGTQTGSSSSFEHMSQEGFSAIT 360
Qy 361 SNGLLSTVGSYDWAGGVFLYTSKEKSTFINMTVDSMDNDAYLGAAAAIILNRVQSLV 420
Db 361 SNGLLSTVGSYDWAGGVFLYTSKEKSTFINMTVDSMDNDAYLGAAAAIILNRVQSLV 420
Qy 421 LGAPRYQHIGLVAMFRONTGWESNANVKQIGAYFGASLCSDVDVDSNGSTDVLVIGAP 480
Db 421 LGAPRYQHIGLVAMFRONTGWESNANVKQIGAYFGASLCSDVDVDSNGSTDVLVIGAP 480
Qy 481 HYEQTREGGVSVCLPRGQARWQCDALVYEGQGPWRFGAALTVLGDVNGDKLTDVA 540
Db 481 HYEQTREGGVSVCLPRGQARWQCDALVYEGQGPWRFGAALTVLGDVNGDKLTDVA 540
Qy 541 IGAPGEDNRGAVYLFHGTSGSGISPSHSORISAGSLSPRLQYFGOSLSGGQDLTMDGLV 600
Db 541 IGAPGEDNRGAVYLFHGTSGSGISPSHSORISAGSLSPRLQYFGOSLSGGQDLTMDGLV 600
Qy 601 DLTVGAQGHVLLRSQPVLRVKAIMEFNPREVARNVFECDNDQVVKGEAGEVRVCLHVOK 660
Db 601 DLTVGAQGHVLLRSQPVLRVKAIMEFNPREVARNVFECDNDQVVKGEAGEVRVCLHVOK 660
Qy 661 STRDLREGQIQSVTVYDLDALDGRPHSRVAVNETKSTRQTOVLGLTQTCETLKLQLP 720
Db 661 STRDLREGQIQSVTVYDLDALDGRPHSRVAVNETKSTRQTOVLGLTQTCETLKLQLP 720
Qy 721 NCIEDPVSPVLRNLNFSIVGTPLSAFGNLRPLAEDAQRLLFTALFPPEKNCNDNICODD 780
Db 721 NCIEDPVSPVLRNLNFSIVGTPLSAFGNLRPLAEDAQRLLFTALFPPEKNCNDNICODD 780
Qy 781 LSIITFSFMSLDCLVGGPREFNTVTVRNDGEDSYRTQVTFPPFLDLSYRKVSTLQNR 840
Db 781 LSIITFSFMSLDCLVGGPREFNTVTVRNDGEDSYRTQVTFPPFLDLSYRKVSTLQNR 840
Qy 841 QRSWLACESASSTEVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLKA 900
Db 841 QRSWLACESASSTEVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLKA 900
Qy 901 NVTSENMPRTNKTEFOLELPVKYAVVMVTSHGVSSTKYLNFTASENTSRVMOHQYQVSN 960

Db 901 NVTSENNPRTNKTBFQLELPVKYAVYVMVSHGVSTKYLNTFASENTSRVMQHOYQVSN 960
QY 961 LQORSLPISLVFLVRLNQTVWDRPQVTFSENLSSTCHTKERLPSSHDFLAELRKAPV 1020
Db 961 LQORSLPISLVFLVRLNQTVWDRPQVTFSENLSSTCHTKERLPSSHDFLAELRKAPV 1020
QY 1021 VNCSTAVCQRIQCDIPFFGQIEEFNATLKGNLSFDWYIKTSHNHLIIYSTABILFNDVSF 1080
Db 1021 VNCSTAVCQRIQCDIPFFGQIEEFNATLKGNLSFDWYIKTSHNHLIIYSTABILFNDVSF 1080
QY 1081 TLLPGQAFVRSQTKVEPPEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKQYKD 1140
Db 1081 TLLPGQAFVRSQTKVEPPEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKQYKD 1140
QY 1141 MMSEGGPPGAEQ 1153
Db 1141 MMSEGGPPGAEQ 1153

RESULT 7

US-08-943-363-3
; Sequence 3, Application US/08943363
; Patent No. 5837478
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,363
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32684
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1153 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-943-363-3

Query Match 100.0%; Score 5953; DB 2; Length 1153;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALRVLLLTALTTLCHGFNLDTENAMTFQENARGFQCSVVQLQGSRVVVGAPQEI VAAANOR 60
Db 1 MALRVLLLTALTTLCHGFNLDTENAMTFQENARGFQCSVVQLQGSRVVVGAPQEI VAAANOR 60
QY 61 GSLVQCDYSTGSCPEIRLQVPVEAVNMSLGLSLAATSTPPQLLACGPTVHTCSENTYVK 120
Db 61 GSLVQCDYSTGSCPEIRLQVPVEAVNMSLGLSLAATSTPPQLLACGPTVHTCSENTYVK 120
QY 121 GLCFLFGSNLQOQPKPPEALRGCPQEDSDAFLIDGSGSIIPHDFRMRKRFVSTMEOL 180
Db 121 GLCFLFGSNLQOQPKPPEALRGCPQEDSDAFLIDGSGSIIPHDFRMRKRFVSTMEOL 180
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Db 181 KKSCTLFLSMQYSEEFRIHFTFKFQNNPNRSLVKPITQLIGRTHATGIRKVVRELFN 240
QY 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVITPEADREGVIRYVIGVDAPRSEKSRQBL 300
Db 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVITPEADREGVIRYVIGVDAPRSEKSRQBL 300
QY 301 NTIASKPPRDHVFQVNNFEALKTIQNLQREKXFALEGTTGSSSSFEHMSOEGFSAAT 360
Db 301 NTIASKPPRDHVFQVNNFEALKTIQNLQREKXFALEGTTGSSSSFEHMSOEGFSAAT 360
QY 361 SNGPLLLSTVGSYDWAGGVFLYTSKEKSTFINNTRVDSMDNDAYLGYAAAILLRNRVQSLV 420
Db 361 SNGPLLLSTVGSYDWAGGVFLYTSKEKSTFINNTRVDSMDNDAYLGYAAAILLRNRVQSLV 420
QY 421 LGAPRYQHIGLVAMPFRONTGMWESNANVKGTOIGAYFGASLCSVDVDSNGSDDLVLIGAP 480
Db 421 LGAPRYQHIGLVAMPFRONTGMWESNANVKGTOIGAYFGASLCSVDVDSNGSDDLVLIGAP 480
QY 481 HYYEOTRGQGVSVCLPRGQARWQCDAVLGEGQCPMRFGAALTVLGDVNGDKLTQVA 540
Db 481 HYYEOTRGQGVSVCLPRGQARWQCDAVLGEGQCPMRFGAALTVLGDVNGDKLTQVA 540
QY 541 IGAPGEEDNRGAVLPHGTSGSGISPSHSQRIAGSKLSPRLQYFQCSLGGQDLTMDGLV 600
Db 541 IGAPGEEDNRGAVLPHGTSGSGISPSHSQRIAGSKLSPRLQYFQCSLGGQDLTMDGLV 600
QY 601 DLTVGAQGHVLLRSQPVLRVKAIMEFNPREVARNVFECNDQVVKGBAGEVRVCLHVQK 660
Db 601 DLTVGAQGHVLLRSQPVLRVKAIMEFNPREVARNVFECNDQVVKGBAGEVRVCLHVQK 660
QY 661 STRDRLREGQIOSVVTYDLALDSGRPHSRAVFNETKNSRTRQTVLGLTOTCETLKLQLP 720
Db 661 STRDRLREGQIOSVVTYDLALDSGRPHSRAVFNETKNSRTRQTVLGLTOTCETLKLQLP 720
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Db 721 NCIEDPVSPIVLRNLNFSLVGTPLSAFGNLRPVLAEADQRLFTALPFFKNCNCNDNICODD 780
QY 781 LSITFSFMSLDCLVVGGRPREFNVTVVRNDEGDSYRTQVTFPPFLDLSYRKVSTLQNRS 840
Db 781 LSITFSFMSLDCLVVGGRPREFNVTVVRNDEGDSYRTQVTFPPFLDLSYRKVSTLQNRS 840
QY 841 QRSWRLACESASSTEVSGALKSTSCSINHPIFPENSEVTNITFPDVSFKASLGNKLLKA 900
Db 841 QRSWRLACESASSTEVSGALKSTSCSINHPIFPENSEVTNITFPDVSFKASLGNKLLKA 900
QY 901 NVTSENNPRTNKTBFQLELPVKYAVYVMVSHGVSTKYLNTFASENTSRVMQHOYQVSN 960
Db 901 NVTSENNPRTNKTBFQLELPVKYAVYVMVSHGVSTKYLNTFASENTSRVMQHOYQVSN 960
QY 961 LQORSLPISLVFLVRLNQTVWDRPQVTFSENLSSTCHTKERLPSSHDFLAELRKAPV 1020
Db 961 LQORSLPISLVFLVRLNQTVWDRPQVTFSENLSSTCHTKERLPSSHDFLAELRKAPV 1020
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Db 1021 VNCSTAVCQRIQCDIPFFGQIEEFNATLKGNLSFDWYIKTSHNHLIIYSTABILFNDVSF 1080

Qy 1081 TLLPQGAFAVSQETKVEPPEVNPPLPLIYGVSSVGGLLALLALITAAALYKLGFFKQYKD 1140
Db 1081 TLLPQGAFAVSQETKVEPPEVNPPLPLIYGVSSVGGLLALLALITAAALYKLGFFKQYKD 1140
Qy 1141 MMEGGPPGAEPO 1153
Db 1141 MMEGGPPGAEPO 1153
RESULT 8
US-09-193-043-3
; Sequence 3, Application US/09193043
; Patent No. 6251395
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 6251395el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT FILING DATE: 1998-11-16
; EARLIER APPLICATION NUMBER: US/09/193,043
; EARLIER FILING DATE: 1993-12-23
; EARLIER APPLICATION NUMBER: 08/173,497
; EARLIER FILING DATE: 1993-12-23
; EARLIER APPLICATION NUMBER: 08/286,889
; EARLIER FILING DATE: 1994-08-05
; EARLIER APPLICATION NUMBER: 08/362,652
; EARLIER FILING DATE: 1994-12-21
; EARLIER APPLICATION NUMBER: 08/943,363
; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-193-043-3
Query Match 100.0%; Score 5953; DB 3; Length 1153;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MALRVLLLTALTLCHGFNLDTENAMTFQENARGFQGVVQLQGSRVVVGAPQEIIVAAQR 60
Db 1 MALRVLLLTALTLCHGFNLDTENAMTFQENARGFQGVVQLQGSRVVVGAPQEIIVAAQR 60
Qy 61 GSYQCDYSTGSCPIRLQVPVEAVNMSLGLSLAATTSPOLLACGPTVHQTCSNTYVK 120
Db 61 GSYQCDYSTGSCPIRLQVPVEAVNMSLGLSLAATTSPOLLACGPTVHQTCSNTYVK 120
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Db 121 GLCFLFGSNLRQOPKQFPPEALRGCPQEDSDIAFLIDGSGSIIPHDFRMRKEFVSTVMEQL 180
Qy 181 KSKTLFSLMQYSEEFHFTFKEFQNNPNRSLVKPITOLLGRTHATGIRKVVRELFN 240
Db 181 KSKTLFSLMQYSEEFHFTFKEFQNNPNRSLVKPITOLLGRTHATGIRKVVRELFN 240
Qy 241 ITNGARKNAFKTLVITDGEKFDPLGYEDVTPEDAREGVIRYVIGVDAPRSEKSRQEL 300
Db 241 ITNGARKNAFKTLVITDGEKFDPLGYEDVTPEDAREGVIRYVIGVDAPRSEKSRQEL 300
Qy 301 NTIASKPRDRHVQVNNFEALKTIQNLREKXFAIEGTQGTSSSSFEHMSQEGFSAAIT 360
Db 301 NTIASKPRDRHVQVNNFEALKTIQNLREKXFAIEGTQGTSSSSFEHMSQEGFSAAIT 360
Qy 361 SNGPLSTVGSVDWAGGVFLYTSKSKSTFINNTRVDSMDNDAYLGAAAILRNVRQSLV 420
Db 361 SNGPLSTVGSVDWAGGVFLYTSKSKSTFINNTRVDSMDNDAYLGAAAILRNVRQSLV 420
Qy 421 LGAPRYQHILGVAMFRONTGMWESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLIGAP 480
Db 421 LGAPRYQHILGVAMFRONTGMWESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLIGAP 480
Qy 481 HYYEOTRGQSVSVCLPRGQARWQCDVLYGEOQGPWGRFGAALTIVLGDVNGDKLTDVA 540

Db 481 HYYEOTRGQSVSVCLPRGQARWQCDVLYGEOQGPWGRFGAALTIVLGDVNGDKLTDVA 540
Qy 541 IGAPGEEDNRGAVLFGHTSGSISPSHSORISAGSKLSPLQYFGOSISGGQDLTMDGLV 600
Db 541 IGAPGEEDNRGAVLFGHTSGSISPSHSORISAGSKLSPLQYFGOSISGGQDLTMDGLV 600
Qy 601 DLTVGAQGHVLLRSLRQVPLRVKAIMBENPREVARNVFECNDQVVKGEAGEVRVCLHVQK 660
Db 601 DLTVGAQGHVLLRSLRQVPLRVKAIMBENPREVARNVFECNDQVVKGEAGEVRVCLHVQK 660
Qy 661 STRDLREGQIQSVVTDALDSCRPHSRVAVNFNTRKSTRQTOVLGLTQTCETLKLQLP 720
Db 661 STRDLREGQIQSVVTDALDSCRPHSRVAVNFNTRKSTRQTOVLGLTQTCETLKLQLP 720
Qy 721 NCIEDPVSPIVLRNLFSLVGTPLSAFGLNLRPLAEDAQRFLTALPPEKNCNNDNICDD 780
Db 721 NCIEDPVSPIVLRNLFSLVGTPLSAFGLNLRPLAEDAQRFLTALPPEKNCNNDNICDD 780
Qy 781 LSITFSFMSLDCLVVGPPREFNVTVTVRNDGEDSYRTQVTFPPFFLDLSYRKVSTLQORS 840
Db 781 LSITFSFMSLDCLVVGPPREFNVTVTVRNDGEDSYRTQVTFPPFFLDLSYRKVSTLQORS 840
Qy 841 QRSWRLACESASSTEVSGALKSTSCSINHPIPPENSEVTNITFDVDSKASLGNKLLKA 900
Db 841 QRSWRLACESASSTEVSGALKSTSCSINHPIPPENSEVTNITFDVDSKASLGNKLLKA 900
Qy 901 NVTSENMPRTNKTEFOLELPVKYAVVMVTVSHGVSTKYNFTASENTSRVMQHOYQVSN 960
Db 901 NVTSENMPRTNKTEFOLELPVKYAVVMVTVSHGVSTKYNFTASENTSRVMQHOYQVSN 960
Qy 961 LGQRLSPISLVFLVPLVRLNQTVIWDPRQVTFSENLSTCHTKERLPSHSDFLAELRKAPV 1020
Db 961 LGQRLSPISLVFLVPLVRLNQTVIWDPRQVTFSENLSTCHTKERLPSHSDFLAELRKAPV 1020
Qy 1021 VNCIAVCORIQCDDIPFGIOEBEFNATLKNLSFDWIKTSHNHLIIVSTAEILFNDVSF 1080
Db 1021 VNCIAVCORIQCDDIPFGIOEBEFNATLKNLSFDWIKTSHNHLIIVSTAEILFNDVSF 1080
Qy 1081 TLLPQGAFAVSQETKVEPPEVNPPLPLIYGVSSVGGLLALLALITAAALYKLGFFKQYKD 1140
Db 1081 TLLPQGAFAVSQETKVEPPEVNPPLPLIYGVSSVGGLLALLALITAAALYKLGFFKQYKD 1140
Qy 1141 MMEGGPPGAEPO 1153
Db 1141 MMEGGPPGAEPO 1153
RESULT 9
US-09-688-307A-3
; Sequence 3, Application US/09688307A
; Patent No. 6432404
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 6432404el Human Beta-2
; FILE REFERENCE: 27866/36646
; CURRENT APPLICATION NUMBER: US/09/688,307A
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 09/193,043
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/605,672
; PRIOR FILING DATE: 1996-02-22
; PRIOR APPLICATION NUMBER: 08/173,497
; PRIOR FILING DATE: 1993-12-23
; PRIOR APPLICATION NUMBER: 08/286,889
; PRIOR FILING DATE: 1994-08-05
; PRIOR APPLICATION NUMBER: 08/362,652
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/943,363
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patent in Ver. 2.0

; SEQ ID NO 3									
; LENGTH: 1153									
; TYPE: PR									
; ORGANISM: Homo sapiens									
US-09-688-307A-3									
Query Match 100.0%; Score 5953; DB 4; Length 1153;									
Best Local Similarity 99.9%; Pred. No. 0;									
Matches 1152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;									
QY	1	MALRVLLLTALT	TLCHGFNLD	TENAMTF	QENARGF	QSVVQL	QSGRVV	VGAPQEI	VAANOR 60
DB	1	MALRVLLLTALT	TLCHGFNLD	TENAMTF	QENARGF	QSVVQL	QSGRVV	VGAPQEI	VAANOR 60
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DB	61	GSLYQCDYST	GCEPIRLQ	VPVEAV	NMSLGL	SLAAT	SPQ	LLACGPT	VHQTCSNTYVK 120
QY	121	GLCFLFGN	LRQOPK	PFPEAL	RGCQ	QEDSD	IAFL	DGSGS	IIPHDFR
DB	121	GLCFLFGN	LRQOPK	PFPEAL	RGCQ	QEDSD	IAFL	DGSGS	IIPHDFR
QY	181	KSKTFL	FSLMQY	SEFR	IHFT	FKFQ	NNPN	PSLVK	PTITQLGR
DB	181	KSKTFL	FSLMQY	SEFR	IHFT	FKFQ	NNPN	PSLVK	PTITQLGR
QY	241	ITNGARK	NAFKIL	VVITD	GKFGD	PLGYE	DVI	PEAD	REGVIR
DB	241	ITNGARK	NAFKIL	VVITD	GKFGD	PLGYE	DVI	PEAD	REGVIR
QY	301	NTIASK	PRDRH	VFQNN	FEAL	KTION	QREK	FAI	EGTGTG
DB	301	NTIASK	PRDRH	VFQNN	FEAL	KTION	QREK	FAI	EGTGTG
QY	361	SNGPLL	STVGS	YDMAGG	VFLY	TSKES	TFIN	TRVDS	DMNDAY
DB	361	SNGPLL	STVGS	YDMAGG	VFLY	TSKES	TFIN	TRVDS	DMNDAY
QY	421	LGAPYQ	HIGL	VAMFR	QNTG	MMES	NAN	KG	TIGAY
DB	421	LGAPYQ	HIGL	VAMFR	QNTG	MMES	NAN	KG	TIGAY
QY	481	HYEOTR	GQSV	CVPL	PRGQ	RA	WOC	DAV	LYGEO
DB	481	HYEOTR	GQSV	CVPL	PRGQ	RA	WOC	DAV	LYGEO
QY	541	IGAPCE	EDNR	GAV	YLPH	TG	SGS	IG	SPSH
DB	541	IGAPCE	EDNR	GAV	YLPH	TG	SGS	IG	SPSH
QY	601	DLTVGA	QGHV	LLRS	QPV	LR	VKA	IME	FNPRE
DB	601	DLTVGA	QGHV	LLRS	QPV	LR	VKA	IME	FNPRE
QY	661	STRDLR	EGQ	OSV	VTY	D	LALD	SGR	PHSA
DB	661	STRDLR	EGQ	OSV	VTY	D	LALD	SGR	PHSA
QY	721	NCIEDP	VP	PIV	LR	NF	SL	VG	TPLS
DB	721	NCIEDP	VP	PIV	LR	NF	SL	VG	TPLS
QY	781	LSIT	FS	MS	LD	CL	V	GG	PRE
DB	781	LSIT	FS	MS	LD	CL	V	GG	PRE
QY	841	QSRW	LAC	ES	AS	TE	V	G	AL
DB	841	QSRW	LAC	ES	AS	TE	V	G	AL
QY	901	NVT	SENN	PR	T	NK	T	F	Q
DB	901	NVT	SENN	PR	T	NK	T	F	Q

QY	961	LGQSLP	ISLV	FLVP	RLNQ	TVIN	DRPQ	VTSE	NI
DB	961	LGQSLP	ISLV	FLVP	RLNQ	TVIN	DRPQ	VTSE	NI
QY	1021	VNC	STAV	COR	Q	OC	D	IP	FF
DB	1021	VNC	STAV	COR	Q	OC	D	IP	FF
QY	1081	TLL	PCQ	GA	FV	AS	Q	TS	ET
DB	1081	TLL	PCQ	GA	FV	AS	Q	TS	ET
QY	1141	MM	SEGG	PP	CA	BP	Q	1153	
DB	1141	MM	SEGG	PP	CA	BP	Q	1153	

RESULT 10
US-09-350-259-3
; Sequence 3, Application US/09350259
; Patent No. 6620915
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 6620915el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/350,259
; CURRENT FILING DATE: 1999-07-08
; EARLIER APPLICATION NUMBER: 09/193,043
; EARLIER FILING DATE: 1998-11-16
; EARLIER APPLICATION NUMBER: 08/173,497
; EARLIER FILING DATE: 1993-12-23
; EARLIER APPLICATION NUMBER: 08/286,889
; EARLIER FILING DATE: 1994-08-05
; EARLIER APPLICATION NUMBER: 08/362,652
; EARLIER FILING DATE: 1994-12-21
; EARLIER APPLICATION NUMBER: 08/943,363
; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1153
; TYPE: PR
; ORGANISM: Homo sapiens
US-09-350-259-3

Query Match 100.0%; Score 5953; DB 4; Length 1153;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	MALRVLLLTALT	TLCHGFNLD	TENAMTF	QENARGF	QSVVQL	QSGRVV	VGAPQEI	VAANOR 60
DB	1	MALRVLLLTALT	TLCHGFNLD	TENAMTF	QENARGF	QSVVQL	QSGRVV	VGAPQEI	VAANOR 60
QY	61	GSLYQCDYST	GCEPIRLQ	VPVEAV	NMSLGL	SLAAT	SPQ	LLACGPT	VHQTCSNTYVK 120
DB	61	GSLYQCDYST	GCEPIRLQ	VPVEAV	NMSLGL	SLAAT	SPQ	LLACGPT	VHQTCSNTYVK 120
QY	121	GLCFLFGN	LRQOPK	PFPEAL	RGCQ	QEDSD	IAFL	DGSGS	IIPHDFR
DB	121	GLCFLFGN	LRQOPK	PFPEAL	RGCQ	QEDSD	IAFL	DGSGS	IIPHDFR
QY	181	KSKTFL	FSLMQY	SEFR	IHFT	FKFQ	NNPN	PSLVK	PTITQLGR
DB	181	KSKTFL	FSLMQY	SEFR	IHFT	FKFQ	NNPN	PSLVK	PTITQLGR
QY	241	ITNGARK	NAFKIL	VVITD	GKFGD	PLGYE	DVI	PEAD	REGVIR
DB	241	ITNGARK	NAFKIL	VVITD	GKFGD	PLGYE	DVI	PEAD	REGVIR
QY	301	NTIASK	PRDRH	VFQNN	FEAL	KTION	QREK	FAI	EGTGTG
DB	301	NTIASK	PRDRH	VFQNN	FEAL	KTION	QREK	FAI	EGTGTG

Db 301 NTIASKPPDRHVQVNNFEALKTIONQREKIFAIEGTQTGSSSSFEHMSQEGFSAIT 360
Qy 361 SNGPLSTVGSYDAGGVLFTSKSTFINNTRVDSMDNDAYLGAAAAIILNRVQSLV 420
Db 361 SNGPLSTVGSYDAGGVLFTSKSTFINNTRVDSMDNDAYLGAAAAIILNRVQSLV 420
Qy 421 LGAPRYQHIGLVAMPFRONTGMWESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLIGAP 480
Db 421 LGAPRYQHIGLVAMPFRONTGMWESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLIGAP 480
Qy 481 HYEOTRGQGVSVCLPRGQARWQCDVAVLGEQGPWGRFGAALTVLGDVNGDKLTDVA 540
Db 481 HYEOTRGQGVSVCLPRGQARWQCDVAVLGEQGPWGRFGAALTVLGDVNGDKLTDVA 540
Qy 541 IGAPDEEDNRGAVLPHGTSGSGISPSHSQRIAGSKLSPRIQYFGOSLGGODLTMDGLV 600
Db 541 IGAPDEEDNRGAVLPHGTSGSGISPSHSQRIAGSKLSPRIQYFGOSLGGODLTMDGLV 600
Qy 601 DLTVGAQGHVLLRSQVPLRVKAIMFNPREVARNVFCNDQVVKGEAGEVRVCLHVQK 660
Db 601 DLTVGAQGHVLLRSQVPLRVKAIMFNPREVARNVFCNDQVVKGEAGEVRVCLHVQK 660
Qy 661 STRDLREGQIQSVVTVYDALDGRPHSRVAFNETKNSRTRQTVLGLTQTCETLKLQLP 720
Db 661 STRDLREGQIQSVVTVYDALDGRPHSRVAFNETKNSRTRQTVLGLTQTCETLKLQLP 720
Qy 721 NCIEDPVSPVILRNFSLVGTPLSAFGLNRPVLAEADQRLFTALPPEKNCNDNICODD 780
Db 721 NCIEDPVSPVILRNFSLVGTPLSAFGLNRPVLAEADQRLFTALPPEKNCNDNICODD 780
Qy 781 LSITFSFMSLDCVVGVPREFNVTVVRNDGEDSYRTQVTFPPDLDSYRKVSTLQNGRS 840
Db 781 LSITFSFMSLDCVVGVPREFNVTVVRNDGEDSYRTQVTFPPDLDSYRKVSTLQNGRS 840
Qy 841 QRSWLACESASSTEVSGALKSTCSINHPIPPENSEVTFNITFPDVSASLGNKLLIKA 900
Db 841 QRSWLACESASSTEVSGALKSTCSINHPIPPENSEVTFNITFPDVSASLGNKLLIKA 900
Qy 901 NVTSENMPRTNKTQFQLELPVKYAVVMTSHGVSTKYLNFTASENTSRVMOHQYQVSN 960
Db 901 NVTSENMPRTNKTQFQLELPVKYAVVMTSHGVSTKYLNFTASENTSRVMOHQYQVSN 960
Qy 961 LGORSPLISLVLVPLVRLNQTVIDRQPVTFSENLSSTCHTKERLPSSHDFLAELRKAPV 1020
Db 961 LGORSPLISLVLVPLVRLNQTVIDRQPVTFSENLSSTCHTKERLPSSHDFLAELRKAPV 1020
Qy 1021 VNCSTAVCQRIQCDIPFFGIQEEFNATLKGNLSPDWYIKTSHNHLIIVSTAEILFNDVSF 1080
Db 1021 VNCSTAVCQRIQCDIPFFGIQEEFNATLKGNLSPDWYIKTSHNHLIIVSTAEILFNDVSF 1080
Qy 1081 TLLPGQGFVRVRSQTEKVEPFPVNPPLIVGSSVGGLLILALITAAALYKLGFFKQRYKD 1140
Db 1081 TLLPGQGFVRVRSQTEKVEPFPVNPPLIVGSSVGGLLILALITAAALYKLGFFKQRYKD 1140
Qy 1141 NMSEGGPPGAEPQ 1153
Db 1141 NMSEGGPPGAEPQ 1153

RESULT 11
US-08-476-062A-43
; Sequence 43, Application US/08476062A
; Patent No. 587275
; GENERAL INFORMATION:
; APPLICANT: Arnaout, M. Amin
; TITLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY
; TITLE OF INVENTION: RESPONSES WITH BETA2 INTEGRINS
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA

COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,062A
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/216,081
FILING DATE: 21-MAR-1994
APPLICATION NUMBER: 07/637,830
FILING DATE: 04-JAN-1991
APPLICATION NUMBER: 07/539,842
FILING DATE: 18-JUN-1990
APPLICATION NUMBER: 07/212,573
FILING DATE: 28-JUN-1988
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00786/068003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1152 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-476-062A-43

Query Match 99.5%; Score 5922.5; DB 2; Length 1152;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1149; Conservative 1; Mismatches 2; Indels 1; Gaps 1;
Qy 1 MALRVLLLTALTLCCHGNLDNENAMTFQENARGQSVVQLQSGRVVVGAPQEIIVAAQR 60
Db 1 MALRVLLLTALTLCCHGNLDNENAMTFQENARGQSVVQLQSGRVVVGAPQEIIVAAQR 60
Qy 61 GSLYQCDYSTGCEPIRLQVPEAVNMSLGLSLAATTPSPOLLACGPTVHQTCSNTYVK 120
Db 61 GSLYQCDYSTGCEPIRLQVPEAVNMSLGLSLAATTPSPOLLACGPTVHQTCSNTYVK 120
Qy 121 GLCFLFGSNLRQOPKPEALRGCPQEDSDIAFLIDGSGSIIPHDFRMKEFVSTVMSQL 180
Db 121 GLCFLFGSNLRQOPKPEALRGCPQEDSDIAFLIDGSGSIIPHDFRMKEFVSTVMSQL 180
Qy 181 KSKTFLSLMOYSEEFRIHFTFKFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFN 240
Db 181 KSKTFLSLMOYSEEFRIHFTFKFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFN 240
Qy 241 ITGARKNAFKILVITDGEKFGDPLGYEDVPEADREGVIRYVIGVGDAPRSEKSRQEL 300
Db 241 ITGARKNAFKILVITDGEKFGDPLGYEDVPEADREGVIRYVIGVGDAPRSEKSRQEL 300
Qy 301 NTIASKPPDRHVQVNNFEALKTIONQREKIFAIEGTQTGSSSSFEHMSQEGFSAIT 360
Db 301 NTIASKPPDRHVQVNNFEALKTIONQREKIFAIEGTQTGSSSSFEHMSQEGFSAIT 360
Qy 361 SNGPLSTVGSYDAGGVLFTSKSTFINNTRVDSMDNDAYLGAAAAIILNRVQSLV 420
Db 361 SNGPLSTVGSYDAGGVLFTSKSTFINNTRVDSMDNDAYLGAAAAIILNRVQSLV 420
Qy 421 LGAPRYQHIGLVAMPFRONTGMWESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLIGAP 480
Db 421 LGAPRYQHIGLVAMPFRONTGMWESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLIGAP 480
Qy 481 HYEOTRGQGVSVCLPRGQARWQCDVAVLGEQGPWGRFGAALTVLGDVNGDKLTDVA 540

Db 481 HYEOTRGQVSVCLPRG-RARWQCDVLYGEOQPMGRFGAALTVLGDVNGDKLTQVA 539
Qy 541 IGAPGEENRGAVALFHTGSGSISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLV 600
Db 540 IGAPGEENRGAVALFHTGSGSISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLV 599
Qy 601 DLTGAQGHVLLRSQPVLRVKAIMEFNPREVARNVFECDQVVKGEAGEVRVCLHVQK 660
Db 600 DLTGAQGHVLLRSQPVLRVKAIMEFNPREVARNVFECDQVVKGEAGEVRVCLHVQK 659
Qy 661 STRDLRGOIQSVVYDIALDSGRPHRAVNETKNSRTRQTVLGLTQTCETLKLQLP 720
Db 660 STRDLRGOIQSVVYDIALDSGRPHRAVNETKNSRTRQTVLGLTQTCETLKLQLP 719
Qy 721 NCIEDPVSPIVLRNFSVLGTPLSAFGNLRPVLAEDAORLFTALPFFKNCNDNICQDD 780
Db 720 NCIEDPVSPIVLRNFSVLGTPLSAFGNLRPVLAEDAORLFTALPFFKNCNDNICQDD 779
Qy 781 LSITFSMSLDCLVGGPREFNVTVVRNDGDSYRTQVTFPPDLDSYRKVSTLQORS 840
Db 780 LSITFSMSLDCLVGGPREFNVTVVRNDGDSYRTQVTFPPDLDSYRKVSTLQORS 839
Qy 841 QRSWLACESASTVSGALKSTCSINHIPIPENSEVTFNITDVSASLGNKLLKA 900
Db 840 QRSWLACESASTVSGALKSTCSINHIPIPENSEVTFNITDVSASLGNKLLKA 899
Qy 901 NVTSENPRNTKTEFQLELPKYAVVMVTVSHGVSTKYLNFTASENTSRVNMHQYQVSN 960
Db 900 NVTSENPRNTKTEFQLELPKYAVVMVTVSHGVSTKYLNFTASENTSRVNMHQYQVSN 959
Qy 961 LGORSPLSLVPLVRLNQTWIDRPQVTFSENLSSTCHTKERLPSSHDFLAEIRKAPV 1020
Db 960 LGORSPLSLVPLVRLNQTWIDRPQVTFSENLSSTCHTKERLPSSHDFLAEIRKAPV 1019
Qy 1021 VNCSTAVCORIQDIPFGIQEFNATLKGNLSPDWYIKTSHNHLIIVSTABILFNDVSF 1080
Db 1020 VNCSTAVCORIQDIPFGIQEFNATLKGNLSPDWYIKTSHNHLIIVSTABILFNDVSF 1079
Qy 1081 TLLPQOGAFVRQOTETKVEPFPVNPPLPLIVGSSVGGILLLALITAAALYKLGFFRQYKD 1140
Db 1080 TLLPQOGAFVRQOTETKVEPFPVNPPLPLIVGSSVGGILLLALITAAALYKLGFFRQYKD 1139
Qy 1141 MMSEGGPPGAEPQ 1153
Db 1140 MMSEGGPPGAEPQ 1152

RESULT 12
PCT-US96-01314-43
; Sequence 43, Application PC/TUS9601314
; GENERAL INFORMATION:
; APPLICANT: M. Amin Arnaut
; TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
; TITLE OF INVENTION: ANTAGONISTS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/01314
; FILING DATE: 30-JAN-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/380,167

; FILING DATE: 30-JAN-95
; ATTORNEY/AGENT INFORMATION:
; NAME: John W. Freeman
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00786/267001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1152
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
PCT-US96-01314-43

Query Match 99.5%; Score 5922.5; DB 5; Length 1152;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1149; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 1 MALRVLLLTALTTLCHGFNLDTENAMTFQENARGFQSVVQLQGSRVVVGAPQEIIVAANQR 60
Db 1 MALRVLLLTALTTLCHGFNLDTENAMTFQENARGFQSVVQLQGSRVVVGAPQEIIVAANQR 60
Qy 61 GSLYQCDYSTGCEPIRLQVPVEAVNMSLGLSLAATTSPQLLACGPTVHQTCSNTYVK 120
Db 61 GSLYQCDYSTGCEPIRLQVPVEAVNMSLGLSLAATTSPQLLACGPTVHQTCSNTYVK 120
Qy 121 GLCFLFGNLRQOPKPPREALRGCPQEDSDIAFLIDGSGSIIPHDFRMKEFVSTVMEOL 180
Db 121 GLCFLFGNLRQOPKPPREALRGCPQEDSDIAFLIDGSGSIIPHDFRMKEFVSTVMEOL 180
Qy 181 KSKTFLSMLQYSEFRHFHTFKFQNNPNRSLVKPITQLLGRTHATGIRKVVRELPN 240
Db 181 KSKTFLSMLQYSEFRHFHTFKFQNNPNRSLVKPITQLLGRTHATGIRKVVRELPN 240
Qy 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVDGDAFSEKSRQEL 300
Db 241 ITNGARKNAFKILVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVDGDAFSEKSRQEL 300
Qy 301 NTIASKPPRDHVQVNNFEALKTIONLREKXFAIEGTQTCSSSSFEHMSQEGFSAAIT 360
Db 301 NTIASKPPRDHVQVNNFEALKTIONLREKXFAIEGTQTCSSSSFEHMSQEGFSAAIT 360
Qy 361 SNGPLLSVGSYDWAGGVFLYTSKEKSTFINNTRVDSMDNDAYLYGAAAIILRNVRQSLV 420
Db 361 SNGPLLSVGSYDWAGGVFLYTSKEKSTFINNTRVDSMDNDAYLYGAAAIILRNVRQSLV 420
Qy 421 LGAPRYQHIGLVAMPRQNTGMWESNANVKGTOIGAYFGASCLSDVDVDSNGSTDVLIGAP 480
Db 421 LGAPRYQHIGLVAMPRQNTGMWESNANVKGTOIGAYFGASCLSDVDVDSNGSTDVLIGAP 480
Qy 481 HYEOTRGQVSVCLPRGQARWQCDVLYGEOQPMGRFGAALTVLGDVNGDKLTQVA 540
Db 481 HYEOTRGQVSVCLPRG-RARWQCDVLYGEOQPMGRFGAALTVLGDVNGDKLTQVA 539
Qy 541 IGAPGEENRGAVALFHTGSGSISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLV 600
Db 540 IGAPGEENRGAVALFHTGSGSISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLV 599
Qy 601 DLTGAQGHVLLRSQPVLRVKAIMEFNPREVARNVFECDQVVKGEAGEVRVCLHVQK 660
Db 600 DLTGAQGHVLLRSQPVLRVKAIMEFNPREVARNVFECDQVVKGEAGEVRVCLHVQK 659
Qy 661 STRDLRGOIQSVVYDIALDSGRPHRAVNETKNSRTRQTVLGLTQTCETLKLQLP 720
Db 660 STRDLRGOIQSVVYDIALDSGRPHRAVNETKNSRTRQTVLGLTQTCETLKLQLP 719
Qy 721 NCIEDPVSPIVLRNFSVLGTPLSAFGNLRPVLAEDAORLFTALPFFKNCNDNICQDD 780
Db 720 NCIEDPVSPIVLRNFSVLGTPLSAFGNLRPVLAEDAORLFTALPFFKNCNDNICQDD 779

Qy	781	LSITFSFMSLDCLVVGPREFNVTVVRNDCGDSYRTQVTFPPFLDL SYRKVUSTLQNR	840
Db	780	LSITFSFMSLDCLVVGPRESNVTVVRNDCGDSYRTQVTFPPFLDL SYRKVUSTLQNR	839
Qy	841	QSRWLACESASSTEVSALKSTSCSINHPIFPENSEVTNITPDVDSKASLGKNKLLKA	900
Db	840	QSRWLACESASSTEVSALKSTSCSINHPIFPENSEVTNITPDVDSKASLGKNKLLKA	898
Qy	901	NVTSENMMPRNTKTEFOLELPVKYAVVMVTSHGVSVKYLNFTASENTSRVMQHOYQVN	960
Db	900	NVTSENMMPRNTKTEFOLELPVKYAVVMVTSHGVSVKYLNFTASENTSRVMQHOYQVN	959
Qy	961	LGQSRPLSIVFLVPVRLNQTIVWDRPQVTFSENLSTCTHKERLP SHSDFLAELRKAPV	1020
Db	960	LGQSRPPTISLVFLVPVRLNQTIVWDRPQVTFSENLSTCTHKERLP SHSDFLAELRKAPV	1019
Qy	1021	VNCISIANCQRIQCDDIPFGIQEEFNATLKGNSLFDWYIKTSHNHLLIVSTAETILFNDSVF	1080
Db	1020	VNCISIANCQRIQCDDIPFGIQEEFNATLKGNSLFDWYIKTSHNHLLIVSTAETILFNDSVF	1079
Qy	1081	TLLPGQAFVRSQRTETKVEPEFVENPLIIVGSSVGGLLILALITAAIYKLGPPFKROYKD	1140
Db	1080	TLLPGQAFVRSQRTETKVEPEFVENPLIIVGSSVGGLLILALITAAIYKLGPPFKROYKD	1139
Qy	1141	MMSEGGPPGABPQ	1153
Db	1140	MMSEGGPPGABPQ	1152

DECEMBER 13

RESULT 13
E424200 2

5424399-2

;Patent No

; APPL:

TITLE ;

NUMBER:

18

1. 1. 1.

AFI
FTT

III.

;

; API

II ;

AP:

THE

Query Match	99.5%;	Score 5922.5;	DB 6;	Length 1152;
Best Local Similarity	99.7%;	Pred. No. 0;		
Matches 1149;	Conservative 1;	Mismatches 2;	Indels 1;	Gaps 1;
Qy	1	MALRVLLLTALTTLCHGFNLDTENAMTFQENARGFGQSVVQLQSGRVVVGAPQEIIVAANQR	60	
Db	1	MALRVLLLTALTTLCHGFNLDTENAMTFQENARGFGQSVVQLQSGRVVVGAPQEIIVAANQR	60	
Qy	61	GSLYQCYDYSTGCBPIRLQVPVEAVNMSLGLSLAATTSPPOLLACGPTVHQTCSENTVYK	120	
Db	61	GSLYQCYDYSTGCBPIRLQVPVEAVNMSLGLSLAATTSPPOLLACGPTVHQTCSENTVYK	120	
Qy	121	GLCFLFGSNLRQOQKPPPEARLGCQOEDSITAFLLIDGSGSIIPHDFRRKPFVSTVMQOL	180	
Db	121	GLCFLFGSNLRQOQKPPPEARLGCQOEDSITAFLLIDGSGSIIPHDFRRKPFVSTVMQOL	180	
Qy	181	KKSXTLFSLMQYSBEFRTHFTFKFQNNPNRSLVKPITQLLGRTHTATGIRKVVRELFN	240	
Db	181	KKSXTLFSLMQYSBEFRTHFTFKFQNNPNRSLVKPITQLLGRTHTATGIRKVVRELFN	240	
Qy	241	ITNGARKNAFKILVVITDGEKFGDPLGVEDVITPEADREGVIRVYVIGVDAPFSEKSRQEL	300	
Db	241	ITNGARKNAFKILVVITDGEKFGDPLGVEDVITPEADREGVIRVYVIGVDAPFSEKSRQEL	300	
Qy	301	NTIASKPPDRHVFOVNNPEALKTIINQURKXFAIEGTQTGSSSSFEHMSQEGFSAAIT	360	

1
2
3
4
5
6

RESULT 14

US-08-476

; Sequenc

; Patent 1

GENERAL:

APPT.

APPL
ETTY

THE

;

; NUMB.

; CORR:

AD:

```

; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,062A
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/216,081
; FILING DATE: 21-MAR-1994
; APPLICATION NUMBER: 07/637,830
; FILING DATE: 04-JAN-1991
; APPLICATION NUMBER: 07/539,842
; FILING DATE: 18-JUN-1990
; APPLICATION NUMBER: 07/212,573
; FILING DATE: 28-JUN-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00786/068003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-8906
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1163 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-476-062A-44

Query Match 58.8%; Score 3500; DB 2; Length 1163;
Best Local Similarity 61.3%; Pred. No. 2.3e-279;
Matches 699; Conservative 139; Mismatches 297; Indels 6; Gaps 4;

QY 5 VLLTALTALCHGNLDNENAMTFQSNARGFGVQVQLQGSRRVVGAPQBIVAANQSGSLY 64
DB 8 LLLFTALATSLGFLNLTDELTAFTAVDSAGFGVQVYANVWVVGAPQKITAANQTGSLY 67
QY 65 QCDYSTGCEPIRLQVPEAVNMSLGLSLAATSPQLLACGPTVHQCSENYVYGLCF 124
DB 68 QCGYSTGACEPIGLQVPEAVNMSLGLSLAATSPQLLACGPTVHHECGRMVLTGLCF 127
QY 125 LFGSNLRQPOKFPALRGCPQEDSDIAFLIDGSGIIPHDPRMKEFVSTVMEQLKSK 184
DB 128 LLGPT--QLTQRLPVSRQECPRQEQDIVFLIDGSGISSRNFATVMNFVRAVISQFRPS 185
QY 185 TLFLSMOYSEBPIHFTPKFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNG 244
DB 186 TQFLSMQFSNKFQTHFTFEFRTPNSLLASVHQLQGFYTTATAIQNVHRLPHASYG 245
QY 245 ARKNAFKILVITDGEKFDPLGYEDVPEADREGVIRYVIGVDGDAFRSEKSRQBLNTIA 304
DB 246 ARRDATKILVITDGEKFDPLGYEDVPEADREGVIRYVIGVDGDAFRSEKSRQBLNTIA 305
QY 305 SKPPRDHVPQNNFALKTIONLREKPAIBCTGTGSSSSFEHEMSQEGFSAALTSNGP 364
DB 306 SKPSQEHIFKVDFFDALKDIONLREKPAIBCTGTGSSSSFEHEMSQEGFSAALTSNGP 365
QY 365 LLSTVGSVDWAGGVLYTSKESKSTFNNTRVDSDDNDVGLYAAAIILNRNRVQSLVLGAP 424
DB 366 VLGVGSGFTWGGALYPPNMSPTFNMSQENVDNRDSTLGLSTELALWKGVSJVLGAP 425
QY 425 RYQHIGLVAMFRQNTGMWESNANVAGTQIGYFGASLCSVDVDSNGSTDVLVIGAPHYYE 484
DB 426 RYQHTGKAVIFQVSRQWRMKAETVGTQIGSYFGASLCSVDVDSNGSTDVLVIGAPHYYE 485
QY 485 QTRGGQVSVCPPLPRGWR--RWCDDAVLYGEQGHPRGFRGAALTVLGVNGDKLTVVIGAP 544

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DB 486 QTRGGQVSVCPPLPRGWR--RWCDDAVLYGEQGHPRGFRGAALTVLGVNGDKLTVVIGAP 544
QY 545 GEEDNRGAVYLFHGTSGSGISPSHQSRIAGSKLSPLQYFQGSQSGGDLTMDGLVDLTV 604
DB 545 GEEDNRGAVYLFHGTSGSGISPSHQSRIAGSKLSPLQYFQGSQSGGDLTMDGLVDLTV 604
QY 605 GAQGHVLLRSQPLRVKAIMFNPMPREVARNVFECNDQVVGKEAGEVRVCLHVOKSTRD 664
DB 605 GARGQVLLLRTRPVLWVGSMQFIPAEIPRSAFECEQVSEQTLVQSNICLYIDKRSKN 664
QY 665 RLREGQIOSVVTYDLALDSGRPHSAVENFKNSRRROTQVLGLTQTCTETLKLQPCNTE 724
DB 665 LLGSRDLQSSVTLDLALDPGRLSPRATEQETKNSRLSRVRVLGLKAKHNFNLLPSCVE 724
QY 725 DPVSPIVLRNFSVLGTPLSAFGLNLRPVLAEDAQRFLTALPFFERKNCNDNICQDLSIT 784
DB 725 DSVTPITLRLNFTLVGKELLAFRLNLRPMLAALQRYFTASLPFERKNCADHICQDNLGIS 784
QY 785 FPFMSLDCLVGGPREFNVTVVRNDEGDSRTQVTFPFLDLSYRKVSTLQNRQSRSW 844
DB 785 FSPFLKSLVGSNLELNARVWVWMDGDSYGTITTFSSHAPAGLSYRYVAEGQKQQLRSL 844
QY 845 RLACESASSTEVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLKANVTS 904
DB 845 HLTCDSPVG--SQGTWSTSCRINHPIPRGAQITFLATFDVSPKAVJGDRLLLTANVSS 902
QY 905 ENNMPRTNKTEFQLELPVKYAVYVVTSHGVSSTKYLNFAS--ENTSRVQHQYQVSNLQ 963
DB 903 ENNTPRTSKTTFQLELPVKYAVYVVTSHGVSSTKYLNFSESEKESHVAMHRYQVNNLQ 962
QY 964 RSLPISLVLVPLRVINQVWDRPQVTPSENLSSTCTHYKERLPSHSDFLAEURKAPVNC 1023
DB 963 RDLPVISINFVPELVQEAQVWMDVEVSHVQNPSPKRCSEKIAPIAPASDFLAHTKQNPVLD 1022
QY 1024 SIANCORTQCDIPRFGIOEENATLKGNLSPDWYIKTSHNHLIIVSTAELFNDSVFTLL 1083
DB 1023 SIAGCLRFCDVPSFSVQEEELDTLKGNLSPGWVQIILQKVVSVSVABITPDTSVISQL 1082
QY 1084 PQGAFVRSQTSQTVKPEPPEVNPPLPIVSGSSVGGILLALITAALYKLGFFKRYKQKMM 1143
DB 1083 PQGAFVRSQTSQTVKPEPPEVNPPLPIVSGSSVGGILLALITAALYKLGFFKRYKQK 1142
QY 1144 E 1144
DB 1143 E 1143

RESULT 15
PCT-US96-01314-44
; Sequence 44, Application PC/TUS9601314
; GENERAL INFORMATION:
; APPLICANT: M. Amin Arnaout
; TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
; TITLE OF INVENTION: ANTAGONISTS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/01314
; FILING DATE: 30-JAN-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/380,167
; FILING DATE: 30-JAN-95

```

ATTORNEY/AGENT INFORMATION:
NAME: John W. Freeman
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00786/267001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 1163
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PCT-US96-01314-44

Query Match 58.8%; Score 3500; DB 5; Length 1163;
Best Local Similarity 61.3%; Pred. No. 2.3e-279;
Matches 699; Conservative 139; Mismatches 297; Indels 6; Gaps 4;
QY 5 LLLTALTLCHGNLDTENAMTFQENARGFGVQVQLOGSRVVGAPQEIIVAAVNOGRGSLY 64
DB 8 LLLFTALATSLGNLDTELTAFRVDSDAGFVSQVYVAVVVGAPQKITAANTGGGLY 67
QY 65 QCDYSTGSCPIRLQVPVEAVNMSLGLSLAATTSPQLACGPTVHQTCSNTYVKGGLCF 124
DB 68 QCGYSTGACEPIGLQVPPPEAVNMSLGLSLASTTSPQLACGPTVHHECGRNMYLTGLCF 127
QY 125 LFGSNLRQOPKFPALRCCPEDSDIAFLIDGSGIIPHDPRRMEKFEVSTVMEQLKSK 184
DB 128 LIGPT--QLTQLPVSQRQCPQEQDIVFLIDGSGISSRNPNATMNFVRAVISQFORPS 185
QY 185 TLFLSMQVSEEFRIHFTKPEFQNNPNRSLVKPITQLLGRHTATGIRKVVRELENTING 244
DB 186 TQFSLMQFSNKQTHTEFEFRRTNPNLSLASVHQLQGGFTTATAIQNVHRLFHASYG 245
QY 245 ARKNAPKLVITDGEKFDPLGYEDVPEADREGVIRYVIGVGDAFRSEKSRQBELNTIA 304
DB 246 ARRDATKILVITDGGKEDSLDYKDVIPMDAAGIIRYAGVGLAFQNRNSWKELNDIA 305
QY 305 SKPPRDHVFQVNNFEALKTIQNLREKFAIBGTGTGSSSSFEHEMSQEGFSAALITNGP 364
DB 306 SKPSQEHIFKVEDFDALQDIONQLEKFAIBGTGTGSSSSFEHEMSQEGFSAVFTPDGP 365
QY 365 LLSTVGSVDWAGGVFLYTSKESKSTFINMTRVDSMDNDAYLGYAAAIILNRVQSLVLGAP 424
DB 366 VLGA VGSFTWSGAFYLPNNMPTINMSQENVDNEDSYLGYSTELALWKGQSLVLGAP 425
QY 425 RYQHIGLVAMFRONTGMESNANVKGTOIGAYFGASLCSVDVDSNGSTDLLVIGAPHYYE 484
DB 426 RYQHTGKAVIFTQVSRQWRMKAENVGTQIGSYFGASLCSVDVDTGSTDLLVIGAPHYYE 485
QY 485 QTRGGQVSVCPPLRQARWQCDVLYGEOGPWRFGAALTIVLDVNGDKLTDVIGAP 544
DB 486 QTRGGQVSVCPPLRQWR--RWCDAVLYGEOGHPWRFGAALTIVLDVNGDKLTDVIGAP 544
QY 545 GEEDNRGAVYLFHGTSGSGISPSHSQIRAGSKLSPRLQVFGOSLGGODLTWMDGLVDLTV 604
DB 545 GEEENRGAVYLFHGVLPISPSHSQIRAGSKLSPRLQVFGQALSGGQDLTQDGLVDLAV 604
QY 605 GAQGHVLLRQSVPLRVKAIMENFNPVARNVFECDNVQVKGKEAGEVVRVCLHVQKSTRD 664
DB 605 GARGQVLLLRTPVLWVGVMQFIPAEIPRSFAFECREQVWSEQTLVQSNICLYIDKRSKN 664
QY 665 RLREGQISVVTYDLALDGRPHSRVAFNETKSTNRQTQVGLTQTCTETKLQLPNCIE 724
DB 665 LIGSRDLQSSVTDLALDPGLSPRATFQETKRSLSRVRLGLKAHCENFNLLPSQVE 724
QY 725 DPVSPVLRLNPSLVGTPLSAPGNLRPVLAEDAQRLFTALPFPKCNCGNDNICDDLSIT 784
DB 725 DSVTPITLRLNFTLVGKPLAFNRNLPMLAALAQRYFTASLPFEKNCAGADHICQDNIGIS 784
QY 785 FSPMSLDCVLVGGPREFNVTVTRNDGEDSVYRTQVTFPPFLDLSYRKVSTLQNRQSRSW 844

DB 785 FSFPGKSLLVGSNLELNAEVMVWVNDGEDSYGTTTFHSHPAGLSYRYVAEGKQQLRSL 844
QY 845 PLACESASSTEVSGALKSTSCSINHPIFPENSEVTNITFDVDSKASLGNKLLKANVTS 904
DB 845 HLTCDSDAPVG--SQGTWSTSCRIINHLIFRGAQITFLATFDVSPKAVILGDRLLLTANVSS 902
QY 905 ENNMPRTNKTFOLELPVKYAVYVWVTSHGVSTKYLNFTAS-ENTSRVMOHQYOVSNLQ 963
DB 903 ENNTPRTSKTTFQLELPVKYAVYVWVSSHEQFTKYLNFSSESEKESHVAMHRYQVNNLQ 962
QY 964 RSLPISLVLPVRLNQTVIWRDPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVNC 1023
DB 963 RDLPSVINFWVPELVNQEAVMWDEVSHPPQNSLRCSSEKIAPPASDDELAHIQKNPVLD 1022
QY 1024 SIAYCORIQCDIPPPGQEEFNATLKGNLSPDWIKTSHNHLIIVSTAELIENDSVFTLL 1083
DB 1023 SIAGCLRFRCDDVPFSVQOEELDTLKGNLSPGWVRQILQKKVSVVSVABEITFDTSVYSQL 1082
QY 1084 PGQAFVRSQETETKVEPPEVNPPLIYVSSVGGILLALITALYKLGFFKROYKDWMS 1143
DB 1083 PGQAFVRSQETETKVEPPEVNPPLIYVSSVGGILLALITALYKLGFFKROYKDWMS 1142
QY 1144 E 1144
DB 1143 E 1143

Search completed: January 13, 2005, 15:34:33
Job time : 61.4108 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2005, 15:03:32 ; Search time 5.47465 Seconds
(without alignments)
3321.665 Million cell updates/sec

Title: RWHLB-B_COPY_144_332
Perfect score: 966
Sequence: 1 CPQEDSDIAFLIDGSGSIIP.....FQVNNFEALKTIONQLREKX 189

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	966	100.0	1153	1 RWHLB	cell surface glyco
2	746	77.2	1153	2 S0051	leukocyte surface
3	540	55.9	1163	1 RWHLB	cell surface glyco
4	328	34.0	1179	2 A5213	integrin alpha-E c
5	287.5	29.8	1170	2 S03308	cell surface glyco
6	261	27.0	1163	2 I56126	lymphocyte fuction
7	242	25.1	493	2 A33809	cartilage matrix p
8	235	24.3	500	2 S65522	cartilage matrix p
9	232	24.0	496	2 A37979	cartilage matrix p
10	215	22.3	3124	2 A40020	collagen alpha 1(X
11	214.5	22.2	1747	2 A45974	collagen alpha 1(X
12	214.5	22.2	1857	2 S31212	collagen alpha 1(X
13	214.5	22.2	1888	2 S78476	collagen alpha 1(X
14	207.5	21.5	1151	2 A45226	integrin alpha-1 c
15	207.5	21.5	3051	2 S42373	hypothetical prote
16	197.5	20.4	272	2 A53348	integrin alpha-1 c
17	192.5	19.9	1180	2 A35854	integrin alpha-1 c
18	191.5	19.8	741	2 T46488	hypothetical prote
19	188	19.5	929	2 I51027	type XII collagen
20	174.5	18.1	2944	2 A54849	collagen alpha 1(V
21	164	17.0	3176	2 CGHU3A	collagen alpha 3(V
22	162	16.8	3137	2 A37797	collagen alpha 3(V
23	159	16.5	1170	2 I45914	integrin alpha 2 s
24	154	15.9	1181	2 A33998	integrin alpha-2 c
25	149	15.4	1178	2 S44142	VLA-2 protein homo
26	146	15.1	550	2 T23760	hypothetical prote
27	143	14.8	843	2 A40970	undulin 1 - human
28	140.5	14.5	371	2 S32604	collagen alpha 2(V
29	136.5	14.1	763	2 I50807	complement factor

ALIGNMENTS

RESULT 1

RWHLB

cell surface glycoprotein CD11b precursor [validated] - human

N:Alternate names: complement receptor type 3 alpha chain; leukocyte adhesion protein Mac
eukocyte integrin alpha chain; neutrophil adherence receptor alphaM chain

C:Species: Homo sapiens (man)

C:Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text change 09-Jul-2004

C:Accession: A31108; A28915; A41600; A30892; A32218; A46526; A26091; I52567

R:Corbi, A.L.; Kishimoto, T.K.; Miller, L.J.; Springer, T.A.

J. Biol. Chem. 263, 12403-12411, 1988

A:Title: The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, CD11B).

A:Reference number: A31108; MUID:88315033; PMID:2457584

A:Accession: A31108

A:Molecule type: mRNA

A:Residues: 1-1153 <CR>

A:Cross-references: UNIPROT:P11215; GB:J03925; NID:G187284; PIDN:AAA59544.1; PID:G307148
A:Note: part of this sequence was confirmed by protein sequencing

R:Arnaout, M.A.; Gupta, S.K.; Pierce, M.W.; Tenen, D.G.

J. Cell Biol. 106, 2153-2158, 1988

A:Title: Amino acid sequence of the alpha subunit of human leukocyte adhesion receptor Mac-1

A:Reference number: A28915; MUID:88257215; PMID:2454931

A:Accession: A28915

A:Molecule type: mRNA

A:Residues: 1-499,501-965, 'P', 967-1153 <ARN>

A:Cross-references: GB:M18044; GB:J03270; GB:M19664; GB:X07421; NID:G186935; PIDN:AAA594594.1
A:Note: the authors translated the codon TAC for residue 1129 as Thr

R:Shelley, C.S.; Arnaout, M.A.

Proc. Natl. Acad. Sci. U.S.A. 88, 10525-10529, 1991

A:Title: The promoter of the CD11b gene directs myeloid-specific and developmentally regulated

A:Reference number: A41600; MUID:92073318; PMID:1683702

A:Accession: A41600

A:Molecule type: DNA

A:Residues: 1-9 <SHE>

A:Cross-references: GB:M76724; NID:G180018; PIDN:AAA58410.1; PID:G553215

R:Arnaout, M.A.; Remold-O'Donnell, E.; Pierce, M.W.; Harris, P.; Tenen, D.G.

Proc. Natl. Acad. Sci. U.S.A. 85, 2776-2780, 1988

A:Title: Molecular cloning of the alpha-subunit of human and guinea pig leukocyte adhesion

A:Reference number: A94193; MUID:88190151; PMID:2833753

A:Accession: A30892

A:Molecule type: mRNA

A:Residues: 917-1042 <AR2>

A:Cross-references: GB:M18044

R:Hickstein, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J.

Proc. Natl. Acad. Sci. U.S.A. 86, 257-261, 1989

A:Title: cDNA sequence for the alphaM subunit of the human neutrophil adherence receptor

A:Reference number: A32218; MUID:89098893; PMID:2563162

A:Accession: A32218

A:Molecule type: mRNA

A:Residues: 9-1153 <HIC>

A:Cross-references: GB:J04145; NID:G189068; PIDN:AAA59903.1; PID:G386975

N:Alternate names: complement-3 receptor alpha chain
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1989 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: S00551; I59078
R:Pytela, R.
EMBL J. 7, 1371-1378, 1988
A>Title: Amino acid sequence of the murine Mac-1 alpha chain reveals homology with the ir
A:Reference number: S00551; MUID:88312584; PMID:3044779
A:Accession: S00551
A:Molecule type: DNA
A:Residues: 1-1153 <P>
A:Cross-references: UNIPROT:P05555; EMBL:X07640; NID:G52982; PIDN:CAA30479.1; PID:G52983
A>Note: the authors translated the codon CAC for residue 569 as Gln
R:Sastre, L.; Roman, J.M.; Teplov, D.B.; Dreyer, W.J.; Gee, C.E.; Larson, R.S.; Roberts,
Proc. Natl. Acad. Sci. U.S.A. 83, 5644-5648, 1986
A>Title: A partial genomic DNA clone for the alpha subunit of the mouse complement receptor
A:Reference number: I59078; MUID:86287312; PMID:2942940
A:Accession: I59078
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 11-44 <RES>
A:Cross-references: GB:M14293; NID:G198993; PIDN:AAA39484.1; PID:G554193
C:Genetics:
A:Gene: Mac-1
C:Superfamily: cell surface glycoprotein Cdlb; von Willebrand factor type A repeat homol
C:Keywords: cell adhesion; glycoprotein; transmembrane protein
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-1153/Product: leukocyte surface glycoprotein Mac-1 alpha chain #status experimental
F:148-318/Domain: von Willebrand factor type A repeat homology <VMA2>
F:1106-1129/Domain: transmembrane #status predicted <TMM>
Query Match 77.2%; Score 746; DB 2; Length 1153;
Best Local Similarity 77.8%; Pred. No. 8.6e-56;
Matches 147; Conservative 20; Mismatches 22; Indels 0; Gaps 0;
Qy 1 CPQEDSIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTFK 60
Db 144 CPQEDSIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTFN 203
Qy 61 EFQNNPRLSLVKPITQLLGRTHATGIRKVRLEFNTNGARKNAFKILVITDGEKFG 120
Db 204 DFENPSPRSHVSPKILNGRTKTASGIRKVRLEFNTNGARKNAFKILVITDGEKFG 263
Qy 121 DPLGYEDVIPADREGVIRYVIGDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
Db 264 DPLGYEDVIPADREGVIRYVIGDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALNT 323
Qy 181 IQNQLREKX 189
Db 324 IQNQLREKX 332
RESULT 3
RWULC
N:Alternate names: leukocyte adhesion receptor p150,95 alpha chain
C:Species: Homo sapiens (man)
C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C:Accession: A35543; S00864
R:Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A.
J. Biol. Chem. 265, 12750-12751, 1990
A:Reference number: A35543
A:Contents: erratum
A:Accession: A35543
A:Molecule type: DNA
A:Residues: 1-1163 <COR>
A:Cross-references: UNIPROT:P20702
A>Note: this revision to the sequence from reference A35543 includes the carboxyl end
R:Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A.
J. Biol. Chem. 265, 2782-2788, 1990
A>Title: Genomic structure of an integrin alpha subunit, the leukocyte p150,95 molecule
A:Reference number: A35543; MUID:90153906; PMID:2303426
A:Accession: A35543

A>Note: part of this sequence was confirmed by protein sequencing
R:Fleming, J.C.; Fahh, H.L.; Gonzalez, D.A.; Smith, T.F.; Tenen, D.G.
J. Immunol. 150, 480-490, 1993
A>Title: Structural analysis of the Cdlb gene and phylogenetic analysis of the alpha-in
n during evolution.
A:Reference number: A46526; MUID:93123748; PMID:8419480
A:Accession: A46526
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-499,501-1153 <PLE>
A:Cross-references: GB:S52227; NID:G263047; PIDN:AB24821.1; PID:G263049
A>Note: the last three bases of intron 13, CAG, are included in some but not all mature
A>Note: sequence extracted from NCBI backbone (NCBIIP:121963)
R:Pierce, M.W.; Renold-O'Donnell, E.; Todd III, R.F.; Arnaout, M.A.
Biochim. Biophys. Acta 874, 368-371, 1986
A>Title: N-terminal sequence of human leukocyte glycoprotein Mol: conservation across sp
A:Reference number: A90664; MUID:87076671; PMID:3539202
A:Accession: A26091
A:Molecule type: protein
A:Residues: 17-31 <PIE>
A:Experimental source: granulocytes
R:Fahh, H.L.; Rosmarin, A.G.; Tenen, D.G.
Blood 79, 865-870, 1992
A>Title: Characterization of the myeloid-specific Cdlb promoter.
A:Reference number: I52567; MUID:92144986; PMID:1346576
A:Accession: I52567
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-9 <RES>
A:Cross-references: GB:M84477; NID:G180184; PIDN:AAA51960.1; PID:G553219
C:Comment: A common beta chain (CD18) forms a heterodimer with this chain to form Mac-1
C:Genetics:
A:Gene: ITGAM; CR3A
A:Cross-references: GDB:120599; OMIM:120980
A:Map position: 16p11.2-16p11.2
A>Note: promoter contains a GATA motif and two Sp1 consensus binding sites
C:Superfamily: cell surface glycoprotein Cdlb; von Willebrand factor type A repeat homol
C:Keywords: alternative splicing; calcium; cell adhesion; glycoprotein; heterodimer; mag
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-1153/Product: cell surface glycoprotein Cdlb #status experimental <MAT>
F:17-1108/Domain: extracellular #status predicted <EXT>
F:148-318/Domain: von Willebrand factor type A repeat homology <VMA2>
F:465-473/Region: calcium/magnesium binding #status predicted
F:530-538/Region: calcium/magnesium binding #status predicted
F:593-601/Region: calcium/magnesium binding #status predicted
F:1109-1134/Domain: transmembrane #status predicted <TMM>
F:1135-1153/Domain: intracellular #status predicted <INT>
F:86,240,391,469,693,735,802,881,901,912,941,947,979,994,1022,1045,1051,1076/Binding
Query Match 100.0%; Score 966; DB 1; Length 1153;
Best Local Similarity 99.5%; Pred. No. 1.2e-74;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CPQEDSIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTFK 60
Db 144 CPQEDSIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTFK 203
Qy 61 EFQNNPRLSLVKPITQLLGRTHATGIRKVRLEFNTNGARKNAFKILVITDGEKFG 120
Db 204 DFENPSPRSHVSPKILNGRTKTASGIRKVRLEFNTNGARKNAFKILVITDGEKFG 263
Qy 121 DPLGYEDVIPADREGVIRYVIGDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
Db 264 DPLGYEDVIPADREGVIRYVIGDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALNT 323
Qy 181 IQNQLREKX 189
Db 324 IQNQLREKX 332
RESULT 2
S00551
leukocyte surface glycoprotein Mac-1 alpha chain precursor - mouse

A:Molecule type: DNA
A:Residues: 1-834 <CO2>
A>Note: this sequence has been revised in reference A36584
R:Corbi, A.L.; Miller, L.J.; O'Connor, K.; Larson, R.S.; Springer, T.A.
EMBO J. 6, 4023-4028, 1987
A:Title: cDNA cloning and complete primary structure of the alpha subunit of a leukocyte
A:Reference number: S00864; MUID:88166845; PMID:3327687
A:Accession: S00864
A:Molecule type: mRNA
A:Residues: 1-755, 'L', 757-1163 <CO3>
A:CROSS-references: GB:M81695; EMBL:Y00093; NID:9487829; PIDN:AAA59180.1; PID:9487830
A>Note: part of this sequence was confirmed by protein sequencing
C:Comment: A common beta chain (CD18) forms a heterodimer with CD11b to form Mac-1 on my
C:Genetics:
A:Gene: GDB:ITGAX; CD11C
A:CROSS-references: GDB:119758; OMIM:151510
A:Map position: 16p11.2-16p11.2
C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat hom
C:Keywords: calcium, cell adhesion; glycoprotein; heterodimer; magnesium; tandem repeat;
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-1163/Product: cell surface glycoprotein CD11c #status predicted <MAT>
F:20-1107/Domain: extracellular #status predicted <EXT>
F:149-319/Domain: von Willebrand factor type A repeat homology <VMA4>
F:1108-1133/Domain: transmembrane #status predicted <TM>
F:1134-1163/Domain: intracellular #status predicted <INT>
F:161.89,392,697,735,899,939,1050/Binding site: carbohydrate (Aen) (covalent) #status pre
Query Match 55.9%; Score 540; DB 1; Length 1163;
Best Local Similarity 55.6%; Pred. No. 4e-38;
Matches 105; Conservative 35; Mismatches 49; Indels 0; Gaps 0;

Qy 1 CPQEDSDIAFLIDSGSIIIPHDFRMKEFVSTVMEQL--KKSKTFLSLMQYSSEFRIHFTFK 60
Db 145 CPRQEDIVFLIDSGSISRRNFATMNFVRAVISQFORPSTQFSLMQFSNKFQTHFTFE 204
Qy 61 EFQNNPRSLVKPITOLLGRHTATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
Db 205 EFRRTSNPLSLASHVOLGFTYTTATQNVVHRLFHASYGARRDATKILVITDGRKEG 264
Qy 121 DPLGVEDVPEADREGVIRVYIGVDAPFRSEKSRQELNTIASKPPRDHVFVNFEALKT 180
Db 265 DSLDYKDVIPMADAGIIRYALGVGLATQNRNSWELNDIASKPSQEHFKVEDFDALKD 324
Qy 181 IQNLREKX 189
Db 325 IQNLKEKI 333

RESULT 4
A:Title: Integrin alpha-E chain - human
C:Species: Homo sapiens (man)
C>Date: 19-Oct-1995 #sequence_revision 31-Mar-2001 #text_change 09-Jul-2004
C:Accession: A53213
J.Shaw, S.K.; Cepek, K.L.; Murphy, E.A.; Russell, G.J.; Brenner, M.B.; Parker, C.M.
J. Biol. Chem. 269, 6016-6025, 1994
A:Title: Molecular cloning of the human mucosal lymphocyte integrin alpha(E) subunit. Un
A:Reference number: A53213; MUID:94164962; PMID:8119947
A:Accession: A53213
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1179 <SHA>
A:CROSS-references: UNIPROT:P38570; GB:I25851; NID:9457244; PID:9457245
C:Genetics:
A:Gene: GDB:ITGAE
A:CROSS-references: GDB:330801
A:Map position: 17p13
C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat hom
F:199-371/Domain: von Willebrand factor type A repeat homology <VMA3>
Query Match 34.0%; Score 328; DB 2; Length 1179;
Best Local Similarity 38.8%; Pred. No. 6e-20;
Matches 71; Conservative 42; Mismatches 68; Indels 2; Gaps 1;

Qy 6 SDIAFLIDSGSIIIPHDFRMKEFVSTVMEQL--KKSKTFLSLMQYSSEFRIHFTFKBQ 63
Db 201 TEIAIILIDSGSIDPPDFQRAKDFISNNMRNFYKCFECFNALVQYGGVQIOTEFDLRDSQ 260
Qy 64 NNPNRSLVKPITOLLGRHTATGIRKVVRELFNTNGARKNAFKILVITDGEKFGDPL 123
Db 261 DVMAASLARVQNTVQGSVTKTASAMQHVLDSIFTSHSGSRKASKVMVVLTDGGIFEDPL 320
Qy 124 GYEDVPEADREGVIRVYIGVDAPFRSEKSRQELNTIASKPPRDHVFVNFEALKTQN 183
Db 321 NLTIVINSPKQGVVERFAIGVEBPKSARTARELNLIASDDETHAFKVTNYMALDGLLS 380
Qy 184 QLR 186
Db 381 KLR 383

RESULT 5
S03308
N:Alternate names: leukocyte adhesion glycoprotein LFA-1 alpha chain; leukocyte function
C:Species: Homo sapiens (man)
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C:Accession: S03308; A47458; A47565; A48759; S36044
R:Larson, R.S.; Corbi, A.L.; Berman, L.; Springer, T.
J. Cell Biol. 108, 703-712, 1989
A:Title: Primary structure of the leukocyte function-associated molecule-1 alpha subunit:
A:Reference number: S03308; MUID:89139587; PMID:2537322
A:Accession: S03308
A:Molecule type: mRNA
A:Residues: 1-1170 <LAR>
A:CROSS-references: UNIPROT:P20701; UNIPROT:Q9UBC8; EMBL:Y00796; NID:g31421; PIDN:CAA6874
A>Note: part of this sequence was confirmed by protein sequencing
R:Corwell, R.D.; Gollahan, K.A.; Hickette, D.D.
Proc. Natl. Acad. Sci. U.S.A. 90, 4221-4225, 1993
A:Title: Description of the leukocyte function-associated antigen 1 (LFA-1 or CD11a) prom
A:Reference number: A47458; MUID:93248261; PMID:8097887
A:Accession: A47458
A:Molecule type: DNA
A:Residues: 1-20 <COR>
A>Note: sequence extracted from NCBI backbone (NCBIN:130862, NCBIP:130863)
R:Shelley, C.S.; Farokhzad, O.C.; Arnaut, M.A.
Proc. Natl. Acad. Sci. U.S.A. 90, 5364-5368, 1993
A:Title: Identification of cell-specific and developmentally regulated nuclear factors th
A:Reference number: A47565; MUID:93281759; PMID:8099450
A:Accession: A47565
A:Molecule type: DNA
A:Residues: 1-20 <SHE>
A:CROSS-references: GB:M95609
R:Nueda, A.; Lopez-Cabrera, M.; Vara, A.; Corbi, A.L.
J. Biol. Chem. 268, 19303-19311, 1993
A:Title: Characterization of the CD11a (alphaL, LFA-1alpha) integrin gene promoter.
A:Reference number: A48759; MUID:93374910; PMID:8103515
A:Accession: A48759
A:Molecule type: DNA
A:Residues: 1-20 <NUE>
A:CROSS-references: EMBL:Z22804; NID:g311405; PIDN:CAA80461.1; PID:g311406
C:Genetics:
A:Gene: GDB:ITGAL; CD11A
A:CROSS-references: GDB:119757; OMIM:153370
A:Map position: 16p11.2-16p11.2
C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homol
C:Keywords: cell adhesion; cytoskeleton; glycoprotein; heterodimer; surface antigen; tra
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-1170/Product: leukocyte adhesion glycoprotein LFA-1 alpha chain #status predicted <
F:154-317/Domain: von Willebrand factor type A repeat homology <VMA2>
Query Match 29.8%; Score 287.5; DB 2; Length 1170;
Best Local Similarity 32.8%; Pred. No. 1.8e-16;
Matches 62; Conservative 50; Mismatches 70; Indels 7; Gaps 2;

Qy 1 CPQEDSDIAFLIDSGSIIIPHDFRMKEFVSTVMEQLKSKTFLSLMQYSSEFRIHFTFK 60

Db	150	CIKGNVDLVFLFDGSMLSQDPEQKILDFMKDWVKLSNTSYQFAAVQFSTSYKTEFDFS	209
Qy	61	BFQNNPNRSLVKPITQLGRTHTATGIRKVVRELFNITNGARKNAFKILVITGCEKFG	120
Db	210	DYVWKWKDPDALLKHVKHMLLLTNTFGAINVATEVFREELGARPDATKLLIIITDGE--A	267
Qy	121	DPLGYEDVIPADREGVIRYVIGVGDAFRSEKSRQELNITIAKPPDRDHVFQVNNTEALKT	180
Db	268	TDSGNIDAAKD-----IIRYIIGIKHFQTKESQETLHKFPASKPASEFVKILDTPEKLD	322
Qy	181	TQNQLREKX	189
Db	323	LFTELOKKI	331

RESULT 6
I56126
lymphocyte function-associated molecule-1-alpha - mouse
C:Species: Mus musculus (house mouse)
C:date: 28-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: I56126
R:Kaufmann, Y.; Tseng, E.; Springer, T.A.
J. Immunol. 147, 369-374, 1991
A>Title: Cloning of the murine lymphocyte function-associated molecule-1 alpha-subunit
A:Reference number: I56126; MUID:91268576; PMID:2051027
A:Accession: I56126
A:A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-1163 <RES>
A:Cross-references: UNIPROT:P24063; GB:M60778; NID:g198785; PID:AAA39426.1; PID:g198786
C:Genetics:
A:Gene: LFA-1
C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat hom
E:351-315/Domain: von Willebrand factor type A repeat homology <WVAL>

RESULT 7

A33809
cartilage matrix protein precursor - chicken
C/Species: Gallus gallus (chicken)
C/Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004
C/Accession: A33809; A26364
R/Kiss, I.; Deak, F.; Holloway Jr., R.G.; Delius, H.; Meubust, K.A.; Frimberger, E.; Argü
J. Biol. Chem. 264, 8126-8134, 1989
A>Title: Structure of the gene for cartilage matrix protein, a modular protein of the ex
grins, Von Willebrand factor, complement factors B and C2, and epidermal growth factor.
A/Reference number: A33809; MUID:89255246; PMID:2542265
A/Accession: A33809
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-493 <KIS>
A/Cross-references: UNIPROT:P05099; GB:X12346; GB:X12347; GB:X12348; GB:X12349; GB:X1235

R. Argraves, W.S.; Deak, F.; Sparks, K.J.; Kiss, I.; Goetinck, P.F.
Proc. Natl. Acad. Sci. U.S.A. 84, 464-468, 1987
A/Title: Structural analysis of cartilage matrix protein deduced from cDNA.
A/Reference number: A26364; MUID:87092429; PMID:3025875
A/Accession: A26364
A/Molecule type: mRNA
A/Residues: 78-493 <RG>
A/Cross-references: GB:M14792; NID:g211545; PIDN:AAA48695.1; PID:g211546
C/Superfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A repeat
F:37-204/Domain: von Willebrand factor type A repeat homology <VWA1>
F:225-260/Domain: EGF homology <EGF>
F:270-434/Domain: von Willebrand factor type A repeat homology <VWA2>

RESULT 8

S66522 cartilage matrix protein precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C:Accession: S66522

R:Azodi, A.; Hauser, N.; Studer, D.; Paulsson, M.; Hiripi, L.; Bosze, Z.
Eur. J. Biochem. 236, 970-977, 1996

A:Title: Cloning, sequencing and expression analysis of mouse cartilage matrix protein cf

A:Reference number: S66522; MUID:96270751; PMID:8665920

A:Accession: S66522

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-500 <AS2>

A:Cross-references: UNIPROT:P51942; EMBL:U35035; NID:gl163178; PIDN:AAB06521.1; PID:gl163178

C:Genetics:

A:Gene: CMP

C:Superfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A repeat

F:1-29/Domain: signal sequence #status: predicted <SIG>

F:30-500/Product: cartilage matrix protein #status: predicted <MAT>

F:43-210/Domain: von Willebrand factor type A repeat homology <VWA1>

F:231-266/Domain: EGF homology <EGF>

F:277-441/Domain: von Willebrand factor type A repeat homology <VWA2>

[illegible]

F:1756-1838/Domain: fibronectin type III repeat homology <FN3M>
F:1847-1928/Domain: fibronectin type III repeat homology <FN3N>
F:1937-2019/Domain: fibronectin type III repeat homology <FN3O>
F:2028-2110/Domain: fibronectin type III repeat homology <FN3P>
F:2119-2199/Domain: fibronectin type III repeat homology <FN3Q>
F:2207-2294/Domain: fibronectin type III repeat homology <FN3R>
F:2325-2490/Domain: von Willebrand factor type A repeat homology <VWA4>
F:2438-2440/Region: cell adhesion #status predicted
F:2509-2750/Domain: IXP, homologous to NC4 domain of type IX collagen #status predicted
F:2751-2902/Domain: collagenous COL2 #status predicted <COL2>
F:2899-2901/Region: cell attachment (R-G-D) motif
F:2903-2945/Domain: non-collagenous NC2 #status predicted <NC2>
F:2946-3048/Domain: collagenous COL1 #status predicted <COL1>
F:3049-3124/Domain: non-collagenous NC1 #status predicted <NC1>
F:32,1006,1032,1044,1512,1767,2210,2273,2532,2683/Binding site: carbohydrate (Asn) (cov
F:2780,2789,2836,2842,2860,2866,2869,3004,3007/Modified site: hydroxyproline (Pro) #statu

Query Match 22.3%; Score 215; DB 2; Length 3124;
Best Local Similarity 30.6%; Pred. NO. 9.9e-10;
Matches 57; Conservative 37; Mismatches 74; Indels 18; Gaps 4;

QY 6 SDIAFLIDSGSIIPHDFRMKEFVSTWME--QLKKSXTLPSLMQYSEFRHFTFEKQ 63
DB 138 TDLVFLVDGSGVSGNFRYILDFFVALVAFDICEKTRVGVQYSSDTRTEFNLNQYF 197

QY 64 NNPNRSIVKPTQLLGRTHATGIRKVVRELFNITNGARKNAFKILVVITDGERKFGDPL 123
DB 198 RRSLLDALKIPYKGNVTGTEADLYLVKNTFTESAGARKGFPKVAIVITDGKA----- 252

QY 124 GYEDVIPADRE---GVIRYVIGVDAPRSEKSKQELNTIASKPPRDHVFQVNNFEALK 179
DB 253 --QDEVEIPARELNRNIGVEVSLGIAKAA-----DAKELKLIASQPSLKHVFNVANFDGIV 305

QY 180 TIONQL 185
DB 306 DIONEI 311

RESULT 11
A45974
collagen alpha 1(XIV) chain precursor, short form 2 - chicken
N:Alternate names: undulin
C:Species: Gallus gallus (chicken)
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A45974; S30085; S2916; S17035; S20833
R:Gercke, D.R.; Foley, J.W.; Castagnola, P.; Gennari, M.; Dublet, B.; Cancedda, R.; Lin
J. Biol. Chem. 268, 12177-12184, 1993
A:Title: Type XIV collagen is encoded by alternative transcripts with distinct 5' region
nb.
A:Reference number: A45974; MUID:93280195; PMID:8505337
A:Accession: A45974
A:Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 1-1747 <GER>
A:Cross-references: UNIPROT:P32018
A:Experimental source: embryo skin
A>Note: sequence inconsistent with the nucleotide translation
A>Note: sequence extracted from NCBI backbone (NCBI:133364, NCBI:133365)
R:Apte, S.S.
submitted to the EMBL Data Library, March 1992
A:Reference number: S30085
A:Accession: S30085
A:Molecule type: mRNA
A:Residues: 1472-1660 <APT>
A:Cross-references: EMBL:X65122; NID:962871; PIDN:CAA46238.1; PID:9938175
R:Trueb, J.; Trueb, B.
Eur. J. Biochem. 207, 549-557, 1992
A:Title: Type XIV collagen is a variant of undulin.
A:Reference number: S22916; MUID:92339443; PMID:1339349
A:Accession: S22916
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 286-494,'Q',496-834,'A',836-1119,'KL',1122-1402,1409-1439 <TRU>

R:Gordon, M.K.; Castagnola, P.; Dublet, B.; Linenmayer, T.F.; van der Rest, M.; Mayne, F.
Eur. J. Biochem. 201, 333-338, 1991
A:Title: Cloning of a cDNA for a new member of the class of fibril-associated collagens v
A:Reference number: S17035; MUID:92037585; PMID:1935930
A:Accession: S17035
A:Molecule type: mRNA
A:Residues: 1472-1659 <GOR1>
A:Accession: S20833
A:Molecule type: protein
A:Residues: 1551-1570;1593-1599;1639-1667 <GOR2>
C:Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trimer
F:40-204/Domain: von Willebrand factor type A repeat homology <VWA1>
F:236-317/Domain: fibronectin type III repeat homology <FN3A>
F:326-409/Domain: fibronectin type III repeat homology <FN3B>
F:418-498/Domain: fibronectin type III repeat homology <FN3C>
F:507-591/Domain: fibronectin type III repeat homology <FN3D>
F:625-707/Domain: fibronectin type III repeat homology <FN3E>
F:716-798/Domain: fibronectin type III repeat homology <FN3F>
F:806-893/Domain: fibronectin type III repeat homology <FN3G>
F:924-1089/Domain: von Willebrand factor type A repeat homology <VWA2>
F:1111-1352/Domain: non-collagenous NC4 #status predicted <NC4>
F:1511-1553/Domain: non-collagenous NC2 #status predicted <NC2>
F:1554-1659/Domain: triple helical domain COL1 #status predicted <COL1>

Query Match 22.2%; Score 214.5; DB 2; Length 1747;
Best Local Similarity 32.4%; Pred. NO. 5.3e-10;
Matches 61; Conservative 31; Mismatches 85; Indels 11; Gaps 4;

QY 1 CPQEDSDIAFLIDSGSIIPHDFRMKEFV-STV--MEQLKSKXTLPSLMQYSEFRHFT 57
DB 920 CKAARADLVFLVDGSGVSGNFRYILDFFVALVAFDICEKTRVGVQYSSDTRTEF 979

QY 58 TPKFQNNPNRSIVKPTQLLGRTHATGIRKVVRELFNITNGARKNAFKILVVITDGE 117
DB 980 KLNAYKTKETLEALQIAYKGNTKGKAKHAREVLFTGEGMRKGIKPKVLVITDGR 1039

QY 118 KFGDPLGYEDVIPADREGVIRYVIGVDAPRSEKSKQELNTIASKPPRDHVFQVNNFEA 177
DB 1040 SQDD---VNKVSREMQLDGFSFFAIGVADADYS-----ELVNIGSKPSERHVFVDDFDA 1091

QY 178 LKTIONQL 185
DB 1092 FTKIEDEL 1099

RESULT 12
S31212
collagen alpha 1(XIV) chain precursor, short form - chicken
C:Species: Gallus gallus (chicken)
C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 15-Sep-2003
C:Accession: S31212
R:Waelchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B.
Eur. J. Biochem. 212, 483-490, 1993
A:Title: Complete primary structure of chicken collagen XIV.
A:Reference number: S31211; MUID:93185668; PMID:8444186
A:Accession: S31212
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-1857 <WAE>
A:Cross-references: EMBL:X70792; NID:928874; PIDN:CAA50063.1; PID:9288875
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
C:Genetics:
A:Gene: Col14A1
C:Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trimer
F:129-1857/Product: collagen alpha 1(XIV) chain, short form #status predicted <SIG>
F:29-110/Domain: fibronectin type III repeat homology <FN3A>
F:156-320/Domain: von Willebrand factor type A repeat homology <VWA1>
F:352-433/Domain: fibronectin type III repeat homology <FN3B>
F:442-525/Domain: fibronectin type III repeat homology <FN3C>
F:534-614/Domain: fibronectin type III repeat homology <FN3D>
F:623-707/Domain: fibronectin type III repeat homology <FN3E>
F:741-823/Domain: fibronectin type III repeat homology <FN3F>

Db 1096 KUNAYKTKETLLEIAIQIAYKGGNTYGTGAUKHAREVLTFTGEAGRMKGIPKVLVWITDGR 1155

QY 118 KFGDPLGYEDVPEADREGVIRYVIGVGDAFRSEKSRQELNTIASPPRDHVQVNNFEA 177

Db 1156 SQDD--VNVKVSREMQLDGFSPFAIGVADADYS-----ELVNIIGSKPSERHVPFVDDFDA 1207

QY 178 LKTIQNQL 185

Db 1208 FTKIEDEL 1215

RESULT 14

A45226

Integrin alpha-1 chain - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C:Accession: A45226

R:Briseewitz, R.; Epstein, M.R.; Marcantonio, E.E.

J. Biol. Chem. 268, 2989-2996, 1993

A:Title: Expression of native and truncated forms of the human integrin alpha 1

A:Reference number: A45226; MUID:93155124; PMID:8428973

A:Accession: A45226

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-1151 <BRI>

A:Cross-references: UNIPROT:P56199

A:Experimental source: hepatoblastoma cell line HepG2

A:Note: sequence extracted from NCBI backbone (NCBIP:124326)

F:142-317/Domain: von Willebrand factor type A repeat homology <VWAI>

Query Match 21.5%; Score 207.5; DB 2; Length 1151;

Best Local Similarity 29.8%; Pred. No. 1.2e-09;

Matches 57; Conservative 39; Mismatches 84; Indels 11; Gaps 5;

QY 7 DIAFLDGGSGIIPDFRMRKPEFVSTVMEQLK--KSKTLFSLMOYSEEFRIHFTFEFQN 64

Db 144 DIVIVLDGSGNSIYPWD--SVTAFNLDLLKRMIDGPKQTQVGIVQYGENVTHEFNLNKYS 201

QY 65 NPNPRSLVPITQLGR-THTATGIRKVKVRELFNITNGARKNAFKILVWITDGEKFGDPL 123

Db 202 TEEVLVAKKIVQRGGRQTWALTGTARKEATEARGARGVKVMVITDGESH-DNH 260

QY 124 GYEDVPEADREGVIRYVIGVGDAFR-----SKSKRQELNTIASKPPRDHVQVNNFEAL 178

Db 261 RLKKVQIDCEDENIQRF5AILGSYNGNLSTSEKPFVEEIKSIASEPTEKHFNFVSDSLAL 320

QY 179 KTIQNOLREKX 189

Db 321 VTIVKTLGERI 331

RESULT 15

S42373

hypothetical protein T70G5.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-May-2004

C:Accession: S42373

R:Smith, A.

submitted to the EMBL Data Library, March 1994

A:Reference number: S42368

A:Accession: S42373

A:Molecule type: DNA

A:Residues: 1-3051 <SMI>

A:Cross-references: EMBL:230423; NID:g458479; PID:g458485

C:Genetics:

A:introns: 96/1; 166/3; 201/2; 355/1; 404/1; 427/2; 794/1; 892/1; 952/2; 1041/1

F:512-679/Domain: von Willebrand factor type A repeat homology <VWAI>

F:754-793/Domain: fibronectin type II repeat homology <2FI>

F:1201-1244/Domain: EGF homology <EGF>

Query Match 21.5%; Score 207.5; DB 2; Length 3051;

Best Local Similarity 31.5%; Pred. No. 4.2e-09;

Matches 63; Conservative 41; Mismatches 71; Indels 25; Gaps 8;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2005, 15:04:07 ; Search time 39.5668 Seconds
(without alignments)
2748.409 Million cell updates/sec

Title: RWHULB-B_COPY_144_332

Perfect score: 966

Sequence: 1 CPQSDSDIAFLIDSGSIIP.....FQVNNFEALQIQNLREKX 189

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	966	100.0	1152	1	ITAM_HUMAN	P11215 homo sapien
2	778	80.5	920	2	Q28984	Q28984 sus scrofa
3	746	77.2	1153	1	ITAM_MOUSE	P05555 mus musculus
4	719	74.4	1151	2	Q9J130	Q9J130 rattus norv
5	595	61.6	1161	1	ITAD_RAT	Q9GYE7 rattus norv
6	586	60.7	1162	1	ITAD_HUMAN	Q13349 homo sapien
7	583	60.4	205	2	Q63001	Q63001 rattus norv
8	540	55.9	1163	1	ITAX_HUMAN	P20702 homo sapien
9	534	55.3	1188	2	Q6KAS4	Q6KAS4 mus musculus
10	534	55.3	1188	2	BAD21383	Bad21383 mus muscu
11	533	55.2	1169	1	ITAX_MOUSE	Q9QXB4 mus musculus
12	408	42.2	304	2	Q6PG66	Q6PG66 mus musculus
13	408	42.2	304	2	AAH57200	Aah57200 mus muscu
14	344	35.6	895	2	Q9WUF8	Q9WUF8 mus sp. itg
15	344	35.6	1167	2	Q88340	Q88340 rattus norv
16	341	35.3	1038	2	Q8BS01	Q8BS01 mus musculus
17	338	35.0	1167	1	ITAE_MOUSE	Q60577 mus musculus
18	328	34.0	1179	1	ITAE_HUMAN	P38570 homo sapien
19	327	33.9	1160	2	Q8WKF4	Q8WKF4 felis silve
20	323.5	33.5	1167	2	Q88341	Q88341 rattus norv
21	319	33.0	231	2	Q8N882	Q8N882 homo sapien
22	294	30.4	79	2	Q8HY27	Q8HY27 ovine aries
23	294	30.4	79	2	Q8HY41	Q8HY41 bos taurus
24	291.5	30.2	1170	1	ITAL_HUMAN	P20701 homo sapien
25	284.5	29.5	1165	1	ITAL_BOVIN	P61625 bos taurus
26	275	28.5	269	2	Q8OWE9	Q8OWE9 rattus norv
27	264.5	27.4	1196	2	Q9RTF1	Q9RTF1 cyprinus ca
28	261	27.0	1160	2	Q9R200	Q9R200 mus musculus
29	261	27.0	1161	2	Q9WTV4	Q9WTV4 mus musculus
30	261	27.0	1163	1	ITAL_MOUSE	P24063 mus musculus
31	260.5	27.0	1166	2	Q6TYB8	Q6TYB8 bos taurus

32	260.5	27.0	1166	2	AAQ90015	AAQ90015 bos tauru
33	250.5	25.9	1187	2	Q98TF0	Q98TF0 cyprinus ca
34	242	25.1	493	1	CAMA_CHICK	P05099 gallus gall
35	238	24.6	257	2	Q8C270	Q8C270 mus musculu
36	237	24.5	652	2	Q95LI2	Q95LI2 bos taurus
37	235	24.3	500	1	CAMA_MOUSE	P51942 mus musculu
38	235	24.3	500	2	Q8OVN5	Q8OVN5 mus musculu
39	232	24.0	496	1	CAMA_HUMAN	P21941 homo sapien
40	231	23.9	656	2	Q96DT1	Q96DT1 homo sapien
41	231	23.9	678	2	Q9UDN0	Q9UDN0 homo sapien
42	231	23.9	678	2	AAQ88704	AAQ88704 homo sapi
43	231	23.9	693	2	Q96DM8	Q96DM8 homo sapien
44	225.5	23.3	1086	2	Q96HB1	Q96HB1 homo sapien
45	223.5	23.1	956	2	Q99K64	Q99K64 mus musculu

ALIGNMENTS

RESULT 1
ITAM_HUMAN
ID ITAM_HUMAN STANDARD; PRT; 1152 AA.
AC P11215;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor MOI)
DE (Neutrophil adherence receptor).
GN Name=ITGAM; Synonyms=CR3A, CD11B;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88315033; PubMed=2457584;
RA Corbi A.L., Kishimoto T.K., Miller L.J., Springer T.A.;
RT "The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, CD11b) alpha subunit. Cloning, primary structure, and relation to the integrins von Willebrand factor and factor B.";
RL J. Biol. Chem. 263:12403-12411(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88190151; PubMed=2833753;
RA Arnaout M.A., Remold-O'Donnell E., Pierce M.W., Harris P., Tenen D.G.;
RT "Molecular cloning of the alpha subunit of human and guinea pig leukocyte adhesion glycoprotein Mol: Chromosomal localization and homology to the alpha subunits of integrins.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:2776-2780(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88257215; PubMed=2454931;
RA Arnaout M.A., Gupta S.K., Pierce M.W., Tenen D.G.;
RT "Amino acid sequence of the alpha subunit of human leukocyte adhesion receptor Mo1 (complement receptor type 3).";
RL J. Cell Biol. 106:2153-2158(1988).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=93123748; PubMed=8419480;
RA Fleming J.C., Pahl H.L., Gonzalez D.A., Smith T.F., Tenen D.G.;
RT "Structural analysis of the CD11b gene and phylogenetic analysis of the alpha-integrin gene family demonstrate remarkable conservation of genomic organization and suggest early diversification during evolution.";
RL J. Immunol. 150:480-490(1993).
RN [5]
RP SEQUENCE OF 9-1153 FROM N.A.
RX MEDLINE=8909893; PubMed=2563162;
RA Hickey D.D., Hickey M.J., Ozols J., Baker D.M., Back A.L., Roth G.J.;
RT "cDNA sequence for the alpha M subunit of the human neutrophil adherence receptor indicates homology to integrin alpha subunits.";

Proc. Natl. Acad. Sci. U.S.A. 86:257-261(1989).
[6]
SEQUENCE OF 1-9 FROM N.A.
MEDLINE=92073318; PubMed=1683702;
RA Shelley C.S., Arnaout M.A.;
RT "The promoter of the CD11b gene directs myeloid-specific and
developmentally regulated expression.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:10525-10529(1991).
[7]
SEQUENCE OF 1-9 FROM N.A.
TISSUE=Blood;
RX MEDLINE=92144986; PubMed=1346576;
RA Pahl H.B., Rosemarin A.G., Tenen D.G.;
RT "Characterization of the myeloid-specific CD11b promoter.";
RL Blood 79:865-870(1992).
[8]
SEQUENCE OF 17-31.
RX MEDLINE=87076671; PubMed=3539202;
RA Pierce M.W., Remold-O'Donnell B., Todd R.F. III, Arnaout M.A.;
RT "N-terminal sequence of human leukocyte glycoprotein Mol: conservation
across species and homology to platelet IIb/IIIa.";
RL Biochim. Biophys. Acta 874:368-371(1986).
[9]
X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 148-331.
RX MEDLINE=95171458; PubMed=7867070;
RA Lee J.O., Kieu P., Arnaout M.A., Liddington R.;
RT "Crystal structure of the A domain from the alpha subunit of integrin
CR3 (CD11b/CD18).";
RL Cell 80:631-638(1995).
[10]
X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 148-334.
RX MEDLINE=96363671; PubMed=8747460;
RA Lee J.O., Bankston L.A., Arnaout M.A., Liddington R.C.;
RT "Two conformations of the integrin A-domain (I-domain): a pathway for
activation?";
RL Structure 3:1333-1340(1995).
[11]
X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 148-337.
RX MEDLINE=98362595; PubMed=9687375;
RA Baldwin E.T., Sarver R.W., Bryant G.L. Jr., Curry K.A.,
FA Fairbanks M.B., Finzel B.C., Garlick R.L., Heinrikson R.L.,
RA Horton N.C., Kelley L.L., Milder A.M., Moon J.B., Mott J.E.,
RA Mutchler V.T., Tomich C.S., Watenpaugh K.D., Wiley V.H.;
RT "Cation binding to the integrin CD11b I domain and activation model
assessment.";
RL Structure 6:923-935(1998).
[12]
3D-STRUCTURE MODELING OF 17-616.
RX MEDLINE=98226734; PubMed=9560195;
RA Oxvig C., Springer T.A.;
RT "Experimental support for a beta-propeller domain in integrin alpha-
subunits and a calcium binding site on its lower surface.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:4870-4875(1998).
CC -I- FUNCTION: Integrin alpha-M/beta-2 is implicated in various
adhesive interactions of monocytes, macrophages and granulocytes
as well as in mediating the uptake of complement-coated particles.
It is identical with CR-3, the receptor for the iC3b fragment of
the third complement component. It probably recognizes the R-G-D
peptide in C3b. Integrin alpha-M/beta-2 is also a receptor for
fibrinogen, factor X and ICAM1. It recognizes P1 and F2 peptides
of fibrinogen gamma chain.
CC -I- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-M
associates with beta-2.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- TISSUE SPECIFICITY: Predominantly expressed in monocytes and
granulocytes.
CC -I- DOMAIN: The integrin I-domain (insert) is a VWF domain. Integrins
with I-domains do not undergo protease cleavage.
CC -I- SIMILARITY: Belongs to the integrin alpha chain family.
CC -I- SIMILARITY: Contains 7 FG-GAP repeats.
CC -I- SIMILARITY: Contains 1 VWF domain.
CC -I- DATABASE: NAME=PROW; NOTE=CD guide CD11b entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd11b.htm".

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EMBL; J03925; AAA59544.1; --
EMBL; M18044; AAA59491.1; --
EMBL; J04145; AAA59903.1; --
EMBL; S52227; AAB24821.1; --
EMBL; S52152; AAB24821.1; JOINED.
EMBL; S52153; AAB24821.1; JOINED.
EMBL; S52154; AAB24821.1; JOINED.
EMBL; S52155; AAB24821.1; JOINED.
EMBL; S52157; AAB24821.1; JOINED.
EMBL; S52159; AAB24821.1; JOINED.
EMBL; S52161; AAB24821.1; JOINED.
EMBL; S52164; AAB24821.1; JOINED.
EMBL; S52165; AAB24821.1; JOINED.
EMBL; S52167; AAB24821.1; JOINED.
EMBL; S52169; AAB24821.1; JOINED.
EMBL; S52170; AAB24821.1; JOINED.
EMBL; S52173; AAB24821.1; JOINED.
EMBL; S52174; AAB24821.1; JOINED.
EMBL; S52180; AAB24821.1; JOINED.
EMBL; S52181; AAB24821.1; JOINED.
EMBL; S52184; AAB24821.1; JOINED.
EMBL; S52189; AAB24821.1; JOINED.
EMBL; S52191; AAB24821.1; JOINED.
EMBL; S52192; AAB24821.1; JOINED.
EMBL; S52203; AAB24821.1; JOINED.
EMBL; S52212; AAB24821.1; JOINED.
EMBL; S52213; AAB24821.1; JOINED.
EMBL; S52216; AAB24821.1; JOINED.
EMBL; S52219; AAB24821.1; JOINED.
EMBL; S52220; AAB24821.1; JOINED.
EMBL; S52221; AAB24821.1; JOINED.
EMBL; S52222; AAB24821.1; JOINED.
EMBL; S52226; AAB24821.1; JOINED.
EMBL; M76724; AAA58410.1; --
EMBL; M84477; AAA51960.1; --
PIR; A31108; RWHULB.
PDB; 1A8X; Model; @=17-1152.
PDB; 1BHO; X-ray; 1/2=--.
PDB; 1BHQ; X-ray; 1/2=--.
PDB; 1IDN; X-ray; 1/2=--.
PDB; 1IDO; X-ray; @=140-331.
PDB; 1JLM; X-ray; @=143-334.
PDB; 1MUU; X-ray; A=137-331.
PDB; 1MF7; X-ray; A=144-337.
PDB; 1N9Z; X-ray; A=140-335.
PDB; 1NA5; X-ray; A=144-345.
PDB; 1NA5; X-ray; A=144-345.
Genew; HGNC:6149; ITGAM.
MIM; 120980; --
GO; GO:0008305; C:integrin complex; TAS.
GO; GO:0007155; P:cell adhesion; TAS.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; VWF_A.
Pfam; PF01839; FG-GAP; 3.
Pfam; PF00357; Integrin_alpha; 1.
Pfam; PF00092; VWA; 1.
PRINTS; PR01185; INTEGRINA.
PRINTS; PR00453; VWFADOMAIN.
SMART; SM00191; Int_alpha; 5.
SMART; SM00327; VWA; 1.
PROSITE; PS00242; INTEGRIN_ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
KW 3D-structure; Calcium; Cell
Glycoprotein; Integrin; Magnesium; Receptor; Repeat; Signal;
Transmembrane.
KW


```
FT SIGNAL 1 16 Integrin alpha-M.
FT CHAIN 17 1152

Query Match
Best Local Similarity 100.0%; Score 966; DB 1; Length 1152;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHPFRMKFVSTVMEQLKKSKTLFSLMOYSEFRHFTFK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHPFRMKFVSTVMEQLKKSKTLFSLMOYSEFRHFTFK 203
QY 61 EFQNNPNRSLVKPIPTQLGRTHATGIRKVVRELFTNITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPIPTQLGRTHATGIRKVVRELFTNITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVPEADREGVIRYVIGVDGDAFRSEKSRQELNTIASKPPDRHVFQVNNFEALKT 180
DB 264 DPLGYEDVPEADREGVIRYVIGVDGDAFRSEKSRQELNTIASKPPDRHVFQVNNFEALKT 323
QY 181 IQNQLREKX 189
DB 324 IQNQLREKI 332

RESULT 2
Q28984
ID Q28984 PRELIMINARY; PRT; 920 AA.
AC Q28984;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE CD11b (Fragment).
GN Name=CD11b;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OC NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee J.-K., Schook L.B., Rutherford M.S.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
DR EMBL; U04072; AAB16869.1; -
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR InterPro; IPR000413; Integrin_alpha.
DR InterPro; IPR002035; VWP_A.
DR Pfam; PF01839; FG-GAP; 3.
DR Pfam; PF00092; VWA; 1.
DR PRINTS; PR01185; INTEGRINA.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00327; VWA; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS0234; VWFA; 1.
KW Cell adhesion; Integrin; Transmembrane.
FT NON_TER 1
FT NON_TER 920
FT SEQUENCE 920 AA; 102440 MW; E96CC51E350DD5AC CRC64;

Query Match
Best Local Similarity 80.4%; Score 778; DB 2; Length 920;
Matches 152; Conservative 19; Mismatches 18; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHPFRMKFVSTVMEQLKKSKTLFSLMOYSEFRHFTFK 60
DB 11 CPQEDSDIAFLIDGSGSIIPHPFRMKFVSTVMEQLKKSKTLFSLMOYSEFRHFTFK 70
QY 61 EFQNNPNRSLVKPIPTQLGRTHATGIRKVVRELFTNITNGARKNAFKILVITDGEKFG 120
DB 71 DFKRNPGLLVKPIPTQLGRTHATGIRKVVRELFTNITNGARKNAFKILVITDGEKFG 130
QY 121 DPLGYEDVPEADREGVIRYVIGVDGDAFRSEKSRQELNTIASKPPDRHVFQVNNFEALKT 180
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DB 131 DPLGYEDVPEADREGVIRYVIGVDGDAFRSEKSRQELNTIASKPPDRHVFQVNNFEALKT 190
QY 181 IQNQLREKX 189
DB 191 IQNQLQEXT 199

RESULT 3
ITAM MOUSE
ID ITAM MOUSE STANDARD; PRT; 1153 AA.
AC P05555; Q8CA73;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor MO1).
GN Name=Itgam;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=86312584; PubMed=3044779;
RA Pyteia R.;
RT "Amino acid sequence of the murine Mac-1 alpha chain reveals homology with the integrin family and an additional domain related to von Willebrand factor.";
RL EMBO J. 7:1371-1378(1988).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojibori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Ciothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Gough J.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shinada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita K.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyszewski-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Kohno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [3]
RP SEQUENCE OF 11-45 FROM N.A.
RX STRAIN=BALB/c; TISSUE=Spleen;
RX MEDLINE=86287312; PubMed=2942940;
RA Sastre L., Roman J.M., Teplow D.B., Dreyer W.J., Gee C.E.,
RA Larson R.S., Roberts T.M., Springer T.A.;
RT "A partial genomic DNA clone for the alpha subunit of the mouse complement receptor type 3 and cellular adhesion molecule Mac-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:5644-5648(1986).
RN [4]
```

SEQUENCE OF 17-28.
 RP MEDLINE=85188276; PubMed=3887182;
 RA Springer T.A., Toplew D.B., Dreyer W.J.;
 RT "Sequence homology of the LFA-1 and Mac-1 leukocyte adhesion
 RL glycoproteins and unexpected relation to leukocyte interferon.";
 Nature 314:540-542(1985).
 CC -!- FUNCTION: Integrin alpha-M/beta-2 is implicated in various
 CC adhesive interactions of monocytes, macrophages and granulocytes
 CC as well as in mediating the uptake of complement-coated particles.
 CC It is identical with CR-3, the receptor for the iC3b fragment of
 CC the third complement component. It probably recognizes the R-G-D
 CC peptide in C3b. Integrin alpha-M/beta-2 is also a receptor for
 CC fibrinogen, factor X and ICAM1. It recognizes P1 and P2 peptides
 CC of fibrinogen gamma chain. Alpha-M/beta-2 play a critical role in
 CC mast cell development and in immune complex-mediated
 CC glomerulonephritis. Mice expressing a null mutation of the alpha-M
 CC subunit gene demonstrate increase in neutrophil accumulation, in
 CC response to a impaired degranulation and phagocytosis, events that
 CC apparently accelerate apoptosis in neutrophils. These mice develop
 CC obesity.
 CC -!- SUBUNIT: Heterodimer of an alpha and a beta chain. Alpha-M
 CC associates with beta-2.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P05555-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P05555-2; Sequence=VSP_010473;
 CC Note=No experimental confirmation available;
 CC -!- TISSUE SPECIFICITY: Predominantly expressed in monocytes and
 CC granulocytes.
 CC -!- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins
 CC with I-domains do not undergo protease cleavage.
 CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
 CC -!- SIMILARITY: Contains 7 FG-GAP repeats.
 CC -!- SIMILARITY: Contains 1 VWFA domain.
 CC -----
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 CC -----
 DR EMBL; X07640; CAA30479.1; -;
 DR EMBL; AK039444; BAC30350.1; -;
 DR EMBL; M14293; AAA39484.1; -;
 DR PIR; S00551; S00551.
 DR HSP; P11215; 1BHO.
 DR MGD; MGI:96607; Itgam.
 DR GO; GO:0009897; C:external side of plasma membrane; IDA.
 DR GO; GO:0007155; P:cell adhesion; IMP.
 DR GO; GO:0045123; P:cellular extravasation; IMP.
 DR GO; GO:0030593; P:neutrophil chemotaxis; IMP.
 DR InterPro; IPR000413; Integrin_alpha.
 DR InterPro; IPR002035; VWF A.
 DR Pfam; PF01839; FG-GAP; 3.
 DR Pfam; PF00357; Integrin_alpha; 1.
 DR Pfam; PF00092; VWA; 1.
 DR PRINTS; PR01185; INTEGRINA.
 DR PRINTS; PR00453; VWFADOMAIN.
 DR SMART; SM00191; Int alpha; 5.
 DR SMART; SM00327; VWA; 1.
 DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.
 DR PROSITE; PS50234; VWFA; 1.
 KW Alternative splicing; Calcium; Cell adhesion;
 KW Direct protein sequencing; Glycoprotein; Integrin; Receptor; Repeat;
 KW Signal; Transmembrane.
 FT SIGNAL 1 16
 FT CHAIN 17 1153
 FT DOMAIN 17 1105
 FT Integrin alpha-M.
 FT Extracellular (Potential).

FT	TRANSMEM	1106	1129	Potential.
FT DOMAIN	1130	1153		Cytoplasmic (Potential).
FT REPEAT	31	84		FG-GAP 1.
FT REPEAT	85	163		FG-GAP 2.
FT DOMAIN	164	350		VWFA. 3.
FT REPEAT	337	400		FG-GAP 3.
FT REPEAT	401	452		FG-GAP 4.
FT REPEAT	454	515		FG-GAP 5.
FT REPEAT	517	575		FG-GAP 6.
FT REPEAT	580	632		FG-GAP 7.
FT CA_BIND	465	473		Potential.
FT CA_BIND	529	537		Potential.
FT CA_BIND	592	600		Potential.
FT SITE	1132	1136		GFPR motif.
FT DISULFID	66	73		By similarity.
FT DISULFID	105	123		By similarity.
FT DISULFID	654	711		By similarity.
FT DISULFID	770	776		By similarity.
FT DISULFID	999	1023		By similarity.
FT DISULFID	1028	1033		By similarity.
FT CARBOHYD	58	58		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	86	86		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	391	391		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	696	696		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	734	734		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	772	772		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	801	801		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	881	881		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	907	907		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	941	941		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	980	980		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	994	994		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	1022	1022		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	1045	1045		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	1051	1051		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	1076	1076		N-linked (GlcNAc. .) (Potential).
FT VARSPLIC	453	569		Missing (in isoform 2). /FTId=VSP_010473.
FT CONFLICT	37	37		N -> S (in Ref. 2).
FT CONFLICT	683	683		V -> G (in Ref. 2).
FT SEQUENCE	1153 AA; 127480 MW; 178DB988A5CB0343 CRC64;			
Query Match	77.2%; Score 746; DB 1; Length 1153;			
Best Local Similarity	77.8%; Pred. No. 7.6e-52;			
Matches 147; Conservative 20; Mismatches 22; Indels 0; Gaps 0;				
Qy	1	CPQSDSIAFLIDGSGSTIIPHDFRMKEFVSTVMEQLKSKTFLSLMOYSSEERHETFK	60	
Db	144	CPQESDIVLIDGSGSINNIDFQMKFEFVSTVMEQFKSKTFLSLMQYSEFRHFTFN	203	
Qy	61	EFQNNPNRSLVKPTITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG	120	
Db	204	DFKENPSRSHVSPKQLNGRTKTASGIRKVVRELFHKTNGARENAKILVITDGEKFG	263	
Qy	121	DPLGYEDVIPADREGVIRYVIGVDAPFRSKSQELNTIASKPRDRHVQNNPEALKT	180	
Db	264	DPLDYKDVIPADRAGVIRYVIGVGNAPFNKQSRRELDTIASKPAGEHVQVDNPEALNT	323	
Qy	181	IONQLREKX	189	
Db	324	IONQLQEKI	332	
RESULT 4				
Q9J130	PRELIMINARY;			
ID Q9J130				
AC Q9J130				
DT 01-OCT-2000	(TrEMBLrel. 15, Created)			
DT 01-OCT-2000	(TrEMBLrel. 15, Last sequence update)			
DT 01-MAR-2004	(TrEMBLrel. 26, Last annotation update)			
DE	Integrin beta 2 alpha subunit.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			

```
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RA SEQUENCE FROM N.A.
RA Pathallah D.M. Sr., Zerria K. Jr.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
DR EMBL; AF268593; AAF81280.1; -.
DR HSP; P11215; IBHQ.
DR GO; GO:0008305; C:integrin complex; IEA.
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
DR InterPro; IPR000413; Integrin_alpha.
DR InterPro; IPR002035; VWF A.
DR Pfam; PF01839; FG-GAP; 2.
DR Pfam; PF00357; Integrin_alpha; 1.
DR Pfam; PF00092; VWA; 1.
DR PRINTS; P11185; INTEGRINA.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00191; Int_alpha; 5.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.
DR PROSITE; PS50234; VWF A.
KW Cell adhesion; Integrin; Transmembrane.
SQ SEQUENCE 1151 AA; 126943 MW; 8F785695D4074CA5 CRC64;

Query Match 74.4%; Score 719; DB 2; Length 1151;
Best Local Similarity 74.1%; Pred. No. 1.2e-49;
Matches 140; Conservative 24; Mismatches 25; Indels 0; Gaps 0;

QY 1 CPQEDSIAFLIDSGSIIPHDFRRMKFVSTVMEQLKSKTLFSLMQYSEFRIHFTPK 60
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
144 CQQESNIAFLIDSGSINTIDFQMKFVSTVMDQFQSKTLFSLMQYSEFRTHFTFN 203
QY 61 EFQNNPRLSVKPTTOLLGRTHATGINKVRELFNITNGARKNAFKLVITDGEKFG 120
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
204 DFKRNPDPKSHVRPIQLNGRTKTASGIRKVVRELFQKINGARDNAAKLVITDGEKFG 263
QY 121 DPLGVEDVPEADREGVIRVYGVGDAPRSEKROELNTIASKPPRDHVFQNNFEALKT 180
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
264 DPLNEDVVIPEAEAGIIRVYGVGNFAFKPOSRELDTIASKPAGDHVFDVDFEALNT 323
QY 181 IQNQLREXX 189
Db |||:|||||:
324 IRNQLQEKI 332

RESULT 5
ID ITAD RAT STANDARD; PRT; 1161 AA.
AC Q9QVE7;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Integrin alpha-D precursor.
GN Name=Itgad;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RA SEQUENCE FROM N.A.
RA O'Brien M.W., VanderVieren M., Kilgannon P.D., Dietsch G.,
RA Gallatin W.M.;
RC STRAIN=Sprague-Dawley;
RT "Cloning of rat alpha D, a novel beta 2 integrin.";
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Integrin alpha-D/beta-2 is a receptor for ICAM3 and
CC VCAM1. May play a role in the atherosclerotic process such as
CC clearing lipoproteins from plaques and in phagocytosis of blood-
CC borne pathogens, particulate matter, and senescent erythrocytes
CC from the blood (By similarity).
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Db 146 CPEQMDIAFLIDSGSINORDPAQMKDFVKALMGFASTSTLFLSMQYSNLIKTHFTT 205
Qy 61 EFQNNPNSLVKPIITOLLGRHTATGIRKVVRELENTNGARKNAFKILVITDGEKFG 120
Db 206 EFKNILDPQSLVDPIVOLQGLTYTAGIRTVMEELFHSKNGSRKSAKILLVITDQKYR 265
Qy 121 DPLGYEDVPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
Db 266 DPLEYSDVIPADKAGIIRYALGVGDAFOEPYALKELNTIGSAPPQDHVFKVGNFNAULRS 325
Qy 181 IQNQLREKX 189
Db 326 IQRLQOEKI 334

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RESULT 6

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ITAD_HUMAN
ID ITAD_HUMAN STANDARD; PRT; 1162 AA.
AC Q13349; Q15575; Q15576;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Integrin alpha-D precursor (leukointegrin alpha D) (CD11d) (ADB2).
GN Name=ITGAD;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=96111956; PubMed=8777714;
RA Van der Vieren M., Le Trong H., Wood C.L., Moore P.F., St John T.,
RA Staunton D.E., Gallatin W.M.;
RT "A novel leukointegrin, alpha d beta 2, binds preferentially to ICAM-
RT 3.";
RL Immunity 3:683-690(1995).
RN [2]
SEQUENCE OF 1-235 FROM N.A.
RX MEDLINE=20187620; PubMed=10722744;
RA Noti J.D., Johnson A.K., Dillon J.D.;
RT "Structural and functional characterization of the leukocyte integrin
RT gene CD11d. Essential role of Sp1 and Sp3.";
RL J. Biol. Chem. 275:8959-8969(2000).
RN [3]
SEQUENCE OF 467-537; 571-602; 633-666; 788-834 AND 910-1125 FROM N.A.
RX MEDLINE=96257236; PubMed=8666289;
RA Wong D.A., Davis E.M., LeBeau M., Springer T.A.;
RT "Cloning and chromosomal localization of a novel gene encoding a human
RT beta 2-integrin alpha subunit.";
RL Gene 171:291-294(1996).
RN [4]
INTERACTION WITH VCAM1.
RX MEDLINE=99059842; PubMed=9841932;
RA Grayson M.H., Van der Vieren M., Sterbinsky S.A., Michael Gallatin W.,
RA Hoffman P.A., Staunton D.E., Bochner B.S.;
RT "alphaDbeta2 integrin is expressed on human eosinophils and functions
RT as an alternative ligand for vascular cell adhesion molecule 1 (VCAM-
RT 1).";
RL J. Exp. Med. 188:2187-2191(1998).
RN [5]
INTERACTION WITH VCAM1.
RX MEDLINE=99370002; PubMed=10438935;
RA Van der Vieren M., Crowe D.T., Hoekstra D., Vazeux R., Hoffman P.A.,
RA Grayson M.H., Bochner B.S., Gallatin W.M., Staunton D.E.;
RT "The leukocyte integrin alpha D beta 2 binds VCAM-1: evidence for a
RT binding interface between I domain and VCAM-1.";
RL J. Immunol. 163:1984-1990(1999).
CC -!- FUNCTION: Integrin alpha-D/beta-2 is a receptor for ICAM3 and
CC VCAM1. May play a role in the atherosclerotic process such as
CC clearing lipoproteins from plaques and in phagocytosis of blood-
CC borne pathogens, particulate matter, and senescent erythrocytes
CC

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CC CC from the blood.
CC -!- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-D
CC associates with beta-2.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed moderately on myelomonocytic cell
CC lines and subsets of peripheral blood leukocytes and strongly on
CC tissue-specialized cells, including macrophages foam cells within
CC atherosclerotic plaques, and on splenic red pulp macrophages.
CC -!- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins
CC with I-domains do not undergo protease cleavage.
CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
CC -!- SIMILARITY: Contains 7 FG-GAP repeats.
CC -!- SIMILARITY: Contains 1 VWFA domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U37028; AAB38547.1; -
CC EMBL; U40274; AAB60634.1; -
CC EMBL; U40275; AAB60635.1; -
CC EMBL; U40276; AAB60636.1; -
CC EMBL; U40277; AAB60637.1; -
CC EMBL; U40279; AAB60638.1; -
CC EMBL; U40278; AAB60638.1; JOINED.
CC EMBL; AF187881; AAF62875.1; -
CC HSSP; P11215; 1BHQ.
CC Genew; HGNC:6146; ITGAD.
CC MIM; 602453; -
CC GO; GO:0008305; C:integrin complex; TAS.
CC GO; GO:0016337; P:cell-cell adhesion; NAS.
CC GO; GO:0007160; P:cell-matrix adhesion; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR000413; Integrin_alpha.
CC InterPro; IPR002035; VWF_A.
CC Pfam; PF01839; FG-GAP; 3.
CC Pfam; PF00357; Integrin_alpha; 1.
CC Pfam; PF00092; VWA; 1.
CC PRINTS; PR01185; INTEGRINA.
CC PRINTS; PR00453; VWFADOMAIN.
CC SMART; SM00191; Int_alpha; 5.
CC SMART; SM00327; VWA_1.
CC PROSITE; PS00242; INTEGRIN_ALPHA; 1.
CC PROSITE; PS50234; VWFA; 1.
CC Kew Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
KW Repeat; Signal; Transmembrane.
FT SIGNAL 1 17 Potential.
FT CHAIN 18 1162 Integrin alpha-D.
FT DOMAIN 18 1100 Extracellular (Potential).
FT TRANSMEM 1101 1121 Potential.
FT DOMAIN 1122 1162 Cytoplasmic (Potential).
FT REPEAT 32 85 FG-GAP 1.
FT REPEAT 86 ? FG-GAP 2.
FT REPEAT 150 332 VWFA.
FT DOMAIN 350 400 FG-GAP 3.
FT REPEAT 401 452 FG-GAP 4.
FT REPEAT 454 516 FG-GAP 5.
FT REPEAT 518 576 FG-GAP 6.
FT REPEAT 581 633 FG-GAP 7.
FT CA_BIND 465 473 Potential.
FT CA_BIND 530 538 Potential.
FT CA_BIND 593 601 Potential.
FT SITE 1127 1131 GFFKR motif.
FT DISULFID 67 74 By similarity.
FT DISULFID 106 124 By similarity.
FT DISULFID 655 710 By similarity.
FT DISULFID 769 775 By similarity.
FT DISULFID 846 861 By similarity.
FT DISULFID 994 1018 By similarity.

```


RT and p150,95 leukocyte adhesion proteins.";

RL J. Immunol. 138:2381-2383(1987).

CC -!- FUNCTION: Integrin alpha-X/beta-2 is a receptor for fibrinogen. It recognizes the sequence G-P-R in fibrinogen. It mediates cell-cell interaction during inflammatory responses. It is especially important in monocyte adhesion and chemotaxis.

CC -!- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-X associates with beta-2.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- TISSUE SPECIFICITY: Predominantly expressed in monocytes and granulocytes.

CC -!- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.

CC -!- SIMILARITY: Belongs to the integrin alpha chain family.

CC -!- SIMILARITY: Contains 7 FG-GAP repeats.

CC -!- SIMILARITY: Contains 1 VWFA domain.

CC -!- DATABASE: NAME=PROW; NOTE=CD guide Cdlc entry; WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdlc.htm".

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/) or send an email to license@sib-sib.ch).

CC -----

DR EMBL; M81695; AA559180.1; -;

DR EMBL; M29165; -; NOT ANNOTATED CDS.

DR EMBL; M29487; AA551620.1; ALT SEQ.

DR EMBL; M29482; AA551620.1; JOINED.

DR EMBL; M29483; AA551620.1; JOINED.

DR EMBL; M29484; AA551620.1; JOINED.

DR EMBL; M29485; AA551620.1; JOINED.

DR EMBL; M29486; AA551620.1; JOINED.

DR EMBL; BC038237; AAH38237.1; -;

DR PIR; A36584; RWHUIC.

DR PDB; 1N3V; X-ray; A=141-338.

DR Genew; HGNC:6152; ITGAX.

DR MIM; 151510; -;

DR GO; GO:0008305; C:integrin complex; TAS.

DR GO; GO:0004872; F:receptor activity; TAS.

DR GO; GO:0007155; P:cell adhesion; TAS.

DR GO; GO:0009887; P:organogenesis; TAS.

DR InterPro; IPR000413; Integrin_alpha.

DR InterPro; IPR02035; VWF_A.

DR Pfam; PF01839; FG-GAP; 1.

DR Pfam; PF00357; Integrin_alpha; 3.

DR Pfam; PF00092; VWFA; 1.

DR PRINTS; PR01185; INTEGRINA.

DR PRINTS; PR00453; VWFADOMAIN.

DR SMART; SM00191; Int_alpha; 5.

DR SMART; SM00327; VWFA; 1.

DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.

DR PROSITE; PS50234; VWFA; 1.

KW 3D-structure; Calcium; Cell adhesion; Direct protein sequencing; Glycoprotein; Integrin; Magnesium; Polymorphism; Receptor; Repeat; Signal; Transmembrane.

FT SIGNAL 1 19

FT CHAIN 20 1163

FT DOMAIN 20 1107

FT TRANSMEM 1108 1128

FT DOMAIN 1129 1163

FT REPEAT 34 87

FT REPEAT 88 ?

FT DOMAIN 165 351

FT REPEAT ? 401

FT REPEAT 402 453

FT REPEAT 455 517

FT REPEAT 518 576

FT REPEAT 581 633

FT REPEAT 466 474

FT CA_BIND 530

FT CA_BIND 538

CA_BIND 593 601

SITE 1131 1135

DISULFID 169 76

DISULFID 108 126

DISULFID 655 712

DISULFID 771 777

DISULFID 848 863

DISULFID 998 1022

DISULFID 1027 1032

CARBOHYD 61 61

CARBOHYD 89 89

CARBOHYD 392 392

CARBOHYD 697 697

CARBOHYD 735 735

CARBOHYD 899 899

CARBOHYD 939 939

CARBOHYD 1050 1050

VARIANT 48 48

CONFLICT 209 209

CONFLICT 251 251

CONFLICT 469 469

CONFLICT 490 490

CONFLICT 547 547

CONFLICT 756 756

CONFLICT 819 819

CONFLICT 1161 1163

STRAND 150 157

TURN 160 161

HELIX 164 178

TURN 179 180

TURN 183 185

STRAND 186 193

STRAND 197 201

HELIX 203 208

HELIX 212 216

TURN 217 218

STRAND 226 226

HELIX 228 236

TURN 237 240

HELIX 242 244

TURN 245 245

TURN 248 249

STRAND 251 258

STRAND 263 263

HELIX 269 278

TURN 279 280

STRAND 282 288

HELIX 290 293

TURN 296 297

HELIX 298 304

HELIX 310 312

STRAND 313 316

HELIX 319 325

TURN 326 334

TURN 335 335

SEQUENCE 1163 AA; 127886 MW; 83658A13B5C5DE8F CRC64;

Query Match 55.9%; Score 540; DB 1; Length 1163;

Best Local Similarity 55.6%; Pred. No. 4,2e-35;

Matches 105; Conservative 35; Mismatches 49; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIPHDFRMKFVSTVMEQLKSKTSLSMOYSEEFRIHFTFK 60

DB 145 CPRQEDIVFLIDSGSISSENFATMNFVRAVISQFORPSTQFSLMQFSNKFQHTTFF 204

QY 61 EFQNNPNRSLVKPITOLLGTHATGIRKVVREINLTNGARKNAPILVITDGEKFG 120

DB 205 EFRRTSNPLSLASVHQOQGYTATATQNVHRLFHASYGARRDATKILVITDCKEG 264

QY 121 DPLGYEDVIPADREGVIRYVIGVDADFSEKSRQELNTIASKPPRDHVFQNNPEALK 180

DB 265 DSLDYKDVIPWADAAGIIRYAIGVLAFQNRNSWELNDIASKPSQEHFKVEDFDALKD 324

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QY 181 IQNQLREKX 189
DB 325 IQNQLKEKI 333

RESULT 9
Q6KAS4
ID O6KAS4 PRELIMINARY; PRT; 1188 AA.
AC O6KAS4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MFLJ00114 protein (Fragment).
GN Name=mFLJ00114;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Saga Y., Kitamura H., Nakagawa T., Nagase T., Ohara O., Koga H.;
RT "Prediction of the Coding Sequences of Mouse Homologues of FLJ Genes:
RT The Complete Nucleotide Sequences of 110 Mouse FLJ-Homologous cDNAs
RT Identified by Screening of Terminal Sequences of cDNA Clones Randomly
RT Sampled from Size-Fractionated Libraries.";
RL DNA Res. 11:167-180(2004).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
DR GO; GO:0009897; C:external side of plasma membrane; IDA.
DR InterPro; IPR000413; Integrin_alpha.
DR Pfam; PF01839; FG-GAP; 3.
DR Pfam; PF00357; Integrin_alpha; 1.
DR Pfam; PF00092; VWA; 1.
DR PRINTS; PR01185; INTEGRINA.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00191; Int_alpha; 5.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS00242; INTEGRIN_ALPHA; UNKNOWN_1.
DR PROSITE; PS02334; VWFA; 1.
KW Cell adhesion; Integrin; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 1188 AA; 131248 MW; 88D93107BDBB4178 CRC64;

Query Match 55.3%; Score 534; DB 2; Length 1188;
Best Local Similarity 54.5%; Pred. No. 1.3e-34;
Matches 103; Conservative 33; Mismatches 53; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRRMKEFVSTVMEQLKKSKTLFSLMOYSEEFRIHFTPK 60
DB 165 CPKQDQDVLFLIDGSGSISSTDFEKMDFVKAVMQQLQRPSTFRSLMQPSDFRVHFTFN 224
QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVKVRELFNITNGARKNAFKLIVITDGEKFG 120
DB 225 NFISTSSPLSLDLSVRQLRGYTYTASAIKHVITELFTTQSGARQDATKVLIVITDGRKQG 284
QY 121 DPLGYEDVTPADREGVIRYVIGVDAPFRSEKSRQELNTIATSKPPRDHVFQVNNFEALKT 180
DB 285 DNLSYDSVIPMAEASIIIRYAIGVGKAFYNEHSKQELKAIASMPHSHEVYFVSENFDAKCD 344
QY 181 IQNQLREKX 189
DB 345 IQNQLKEKI 353

RESULT 11
ITAX MOUSE
ID ITAX MOUSE STANDARD; PRT; 1169 AA.
AC Q9QXH4;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Integrin alpha-X precursor (Leukocyte adhesion glycoprotein p150,95
DE alpha chain) (Leukocyte adhesion receptor p150,95) (CD11c).
GN Name=Itgax;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Dendritic cell;
RA Huang X., Gorski K., Tong C., Rattis F.-M., Tseng S.-Y., Pardoll D.,
RA Tsuchiya H.;
RT "Isolation of genes selectively expressed by dendritic cells.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Integrin alpha-X/beta-2 is a receptor for fibrinogen. It
CC recognizes the sequence G-P-R in fibrinogen. It mediates cell-cell
CC interaction during inflammatory responses. It is especially
CC important in monocyte adhesion and chemotaxis (By similarity).
CC -!- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-X
CC associates with beta-2 (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins
CC with I-domains do not undergo protease cleavage.
CC -!- SIMILARITY: Belongs to the integrin alpha chain family.

```

QY	121	DPLGYEDVPEADREGVIRVYIGVGDAFRSEKSRQELNLTASKPPDRDHVFOVNNFEALKT	180
Db	266	DNLSDYSLVPMPEASIIRYALGVGKAFYNEHSKQELKATASMPHSYVFSVENFALKD	325
QY	181	IQNLREKX 189	
Db	326	IQNLREKI 334	
RESULT 12			
Q6PG66			
ID	Q6PG66	PRELIMINARY; PRT; 304 AA.	
AC	Q6PG66;		
DT	05-JUL-2004 (TrEMBLrel. 27, Created)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)		
DE	Integrin alpha X.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
EN	[1]		
SEQUENCE FROM N.A.			
RC	STRAIN=129; TISSUE=Mammary tumor. Brcal-/-fl;		
RX	MEDLINE=223388257; PubMed=12477932;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Schenken C.M., Schuler G.D.,		
RA	Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stowletton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abranson R.D., Mullany S.J.,		
RA	Bosak S.A., McWain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		
RA	Krzywinski M.I., Skalska U., Smalus D.E., Schnerch A., Schein J.E.,		
RA	Jones S.J., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).		
RP	[2]		
SEQUENCE FROM N.A.			
RC	STRAIN=129; TISSUE=Mammary tumor. Brcal-/-fl;		
RC	Strausberg R.;		
RL	Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.		
RL	EMBL, BC057200; AAH57200.1; -		
DR	GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.		
DR	InterPro; IPR002035; VNF_A.		
DR	Pfam; PF00092; VWA; 1.		
DR	PRINTS; PR00453; VNFADOMAIN.		
DR	SMART; SM00327; VWA; 1.		
DR	PROSITE; PS50234; VWFA; 1.		
KW	Integrin.		
SQ	SEQUENCE 304 AA; 33404 MW; EC52F3EA48FA068D CRC64;		
Query Match 42.2%; Score 408; DB 2; Length 304;			
Best Local Similarity 53.3%; Pred. No. 5e-25;			
Matches 80; Conservative 25; Mismatches 43; Indels 2; Gaps 17			
QY	1	CPQEDSIAFLIDSGSIIPHDFRRMKFEFVSTVMEQLKSKTFLSLMOYSEBFRIHFTFK	60
Db	146	CPKQDQDIVLIDSGSGISSTDFEKMLDFVKAVMSQLQRPSTFSLMQFSDFRVHFTFN	205
QY	61	EFQNNPNSRLVPIITOLLGRHTATGIRKVRLEPNITNGARKNAFKILVITDGEKFG	120
Db	206	NFTSTSGPLSLLDSVRLQGYTTAAGIAKHVITELFTTQSGARQDATKVLIVITDGRKQG	265
QY	121	DPLGYEDVPEADREGVIRVYIGVG--DAF 148	

DT	01-NOV-1999	12, Last sequence update)
DT	01-JUN-2003	24, Last annotation update)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2005, 14:59:41 ; Search time 35.3364 Seconds
(without alignments)
1918.696 Million cell updates/sec

Title: RWULB-B_COPY_144_332
Perfect score: 966
Sequence: 1 CPQEDSDIAFLDGGSIIP.....FQVNFALKTIQNQLREKX 189

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_238sep04:.*
1: Geneseq1980s:.*
2: Geneseq1990s:.*
3: Geneseq2000s:.*
4: Geneseq2001s:.*
5: Geneseq2002s:.*
6: Geneseq2003as:.*
7: Geneseq2003bs:.*
8: Geneseq2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	966	100.0	1152	8	ADM99589 Human int
2	966	100.0	1152	8	ADP12435 Protein e
3	966	100.0	1153	2	AAR04136 Alpha sub
4	966	100.0	1153	2	AAR04136 Alpha sub
5	966	100.0	1153	3	AAR65090 Human Bet
6	966	100.0	1153	3	AAR07360 Human CD1
7	966	100.0	1153	5	AAR08252 Human int
8	966	100.0	1153	5	ABG61469 Human Bet
9	966	100.0	1153	5	AAR014428 Integrin
10	960	99.4	1187	2	ADP25615 Binding d
11	956	99.0	191	5	AAY21991 Human com
12	956	99.0	191	5	AAR76856 Human int
13	934	96.7	216	4	AAR76847 Human int
14	934	96.7	435	2	AAR77461 Amino aci
15	893	92.4	177	5	AAR76866 Human int
16	890	92.1	177	5	AAR76865 Human int
17	737	76.3	199	5	ABB78072 Murine I-
18	595	61.6	1151	2	AAR23059 Rat beta
19	595	61.6	1151	2	AAR60001 Rat alpha
20	595	61.6	1151	2	AAR65101 Rat beta-
21	595	61.6	1151	2	AAR72834 Rat alpha
22	595	61.6	1151	2	AAR73344 Rat alpha
23	595	61.6	1151	3	AAR07371 Rat alpha
24	595	61.6	1151	5	ABG61480 Rat Beta2
25	595	61.6	1161	2	AAR78169 Rat alpha

26	595	61.6	1161	2	AAW23062	Aaw23062 Rat beta
27	595	61.6	1161	2	AAW60004	Aaw60004 Rat alpha
28	595	61.6	1161	2	AAW65104	Aaw65104 Rat beta-
29	595	61.6	1161	2	AAW72824	Aaw72824 Rat alpha
30	595	61.6	1161	2	AAW73345	Aaw73345 Rat alpha
31	595	61.6	1161	3	AAW07374	Aaw07374 Rat alpha
32	595	61.6	1161	5	ABG61483	Abg61483 Rat Beta2
33	594	61.5	413	2	AAW23065	Aaw23065 Rabbit be
34	594	61.5	413	2	AAW65107	Aaw65107 Rabbit be
35	594	61.5	413	2	AAW72839	Aaw72839 Rabbit al
36	594	61.5	413	2	AAW73348	Aaw73348 Rabbit al
37	594	61.5	413	3	AAW07377	Aaw07377 Rabbit al
38	594	61.5	1151	2	AAR78179	Aar78179 Rat alpha
39	592	61.3	413	5	ABG61486	Abg61486 Rabbit Be
40	586	60.7	1155	2	AAR78167	Aar78167 Mouse alp
41	586	60.7	1155	2	AAW23060	Aaw23060 Mouse bet
42	586	60.7	1155	2	AAW60002	Aaw60002 Mouse alp
43	586	60.7	1155	2	AAW65102	Aaw65102 Mouse bet
44	586	60.7	1155	2	AAW72835	Aaw72835 Mouse alp
45	586	60.7	1155	2	AAW73346	Aaw73346 Mouse alp

ALIGNMENTS

RESULT 1
ADM99589
ID ADM99589 standard; protein; 1152 AA.
XX
AC ADM99589;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human integrin alphaM subunit precursor protein.
XX
KW integrin alpha subunit; beta; antipsoriatic; thrombolytic; anticoagulant;
KW osteopathic; cytostatic; immunosuppressive; antinflammatory;
KW neuroprotective; antischlicking; immunotherapy; inflammatory;
KW autoimmune disorder; thrombosis; cancer; osteoporosis;
KW sickle cell anaemia; psoriasis; multiple sclerosis; human; precursor;
KW alphas.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 965 /note= "Encoded by CCC"
FT
XX WO2004007530-A2.
XX
PD 22-JAN-2004.
XX
PF 17-JUL-2003; 2003WO-US022301.
XX
PR 17-JUL-2002; 2002US-0396783P.
PR 17-JUL-2002; 2002US-0396790P.
PR 11-SEP-2002; 2002US-0410135P.
XX
PA (BLOO-) CENT BLOOD RES INC.
XX
PI Springer TA, Takagi J;
XX
DR WPI; 2004-122877/12.
XX
DR N-PSDB; ADM99588.
XX
PT Novel modified integrin protein having extracellular domains of integrin
PT alpha and beta subunits or integrin alphaI and beta3 subunit, useful for
PT treating integrin mediated disorders.
XX
PS Disclosure; SEQ ID NO 4; 232pp; English.
XX
CC The invention relates to a novel isolated or recombinant modified
CC integrin protein having extracellular domains of integrin alpha and beta

CC subunits where one of the subunits has one or more mutations, an altered
CC surface feature or an amino acid substitution or internal deletion,
CC extracellular domains of the integrin beta subunit that comprise a
CC mutation that alters a non-cysteine residue to cysteine or extracellular
CC domains of integrin alpha and beta subunits. The polypeptide of the
CC invention demonstrates antiproliferative, thrombolytic, anticoagulant,
CC osteoprotective, cytostatic, immunosuppressive, antiinflammatory,
CC neuroprotective and antitickling activities and may be useful for
CC immunotherapy in order to prevent or treat an integrin-mediated disorder
CC such as an inflammatory disorder, an autoimmune disorder, thrombosis,
CC cancer, osteoporosis, sickle cell anaemia, psoriasis and multiple
CC sclerosis. The current sequence is that of the human integrin alpha
CC subunit precursor protein of the invention.
XX
SQ Sequence 1152 AA;

Query Match 100.0%; Score 966; DB 8; Length 1152;
Best Local Similarity 99.5%; Pred. No. 2.5e-96;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTILFSLMOYSEEFRIHFTFK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTILFSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSKQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSKQELNTIASKPPRDHVFQVNNFEALKT 323
QY 181 IQNQLREKX 189
DB 324 IQNQLREKI 332

RESULT 2
ADP12435
ID ADP12435 standard; protein; 1152 AA.

XX ADP12435;
AC ADP12435;
DT 12-AUG-2004 (first entry)
XX
DE Protein encoded by mRNA of the invention #45.
XX
KW transplant rejection; immune system; rheumatoid arthritis; lupus;
KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS.

XX Homo sapiens.
XX WO2004042346-A2.

XX 21-MAY-2004.
XX 24-APR-2003; 2003WO-US012946.
XX 20-APR-2002; 2002US-00131831.
XX 20-DEC-2002; 2002US-00325899.
XX (EXPR-) EXPRESSION DIAGNOSTICS INC.

XX Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
PI Rosenberg S;
XX WPI; 2004-400724/37.

XX Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT rejection, in an individual, comprises detecting the expression level of
PT the genes.
XX

PS Claim 65; SEQ ID NO 2444; 1762pp; English.
XX
CC The present invention relates to diagnosing or monitoring transplant
CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
CC comprises detecting the expression level of one or more genes. The
CC methods, system and kits are useful in diagnosing or monitoring
CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
CC islet, lung, bone marrow or stem cell transplant rejection,
CC xenotransplant rejection or mechanical organ replacement rejection, in an
CC individual. The method is also useful in assessing the immune status of
CC an individual. The methods are also useful in diagnosing and monitoring
CC diseases that involve the immune system, e.g. rheumatoid arthritis,
CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
CC vital, bacterial or fungal infection. The present sequence represents a
CC protein that is encoded by the mRNA of the invention.
XX
SQ Sequence 1152 AA;

Query Match 100.0%; Score 966; DB 8; Length 1152;
Best Local Similarity 99.5%; Pred. No. 2.5e-96;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTILFSLMOYSEEFRIHFTFK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTILFSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSKQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSKQELNTIASKPPRDHVFQVNNFEALKT 323
QY 181 IQNQLREKX 189
DB 324 IQNQLREKI 332

RESULT 3
AAR04136
ID AAR04136 standard; protein; 1153 AA.

XX AAR04136;
AC AAR04136;
DT 09-SEP-2004 (revised)
DT 25-MAR-2003 (revised)
DT 07-SEP-1990 (first entry)
XX
DE Alpha subunit of Mac-1 leukocyte adhesion receptor.
XX
KW Mac-1 alpha subunit; Mac-1 alpha/beta heterodimer;
KW non-specific defence system; integrin gene superfamily.
XX Synthetic.

XX Key Location/Qualifiers
FH Region 1. 16
FT /label= signal_peptide
FT Modified-site 86. .88
FT /label= putative N-glycosylation site
FT Modified-site 240. .242
FT /label= putative N-glycosylation site
FT Modified-site 391. .393
FT /label= putative N-glycosylation site
FT Modified-site 469. .471
FT /label= putative N-glycosylation site
FT Modified-site 693. .695
FT /label= putative N-glycosylation site
FT Modified-site 697. .699
FT /label= putative N-glycosylation site
FT Modified-site 735. .737
FT /label= putative N-glycosylation site

DB 204 EFQ

121 DFLGIEDVIF EADREGVIRYVIGVGDAFRSEKSRQELNITASKPFRDHFVQVNNFEALKT 180

Db 204 EFQNNPRLSVKPIQLLGRTHATGIRKVVRELFNITNGARKNAFKILVWITDGEKFG 263

CC binding of an integrin to a cognate ligand such as Crohn's disease,
CC nephritis; human immunodeficiency virus (HIV), myocardial infarction,
CC Sjogren's syndrome, rheumatoid arthritis, dermatitis. A therapeutic
CC composition comprising the peptide of the invention is useful for
CC treating an integrin mediated disorder in a subject. The polypeptides
CC and/or active or antigenic fragments are useful as reagents for diagnosis
CC of integrin-mediated disorders. The present sequence represents the human
CC integrin-1 alpha-M protein subunit used to generate the mutant
CC polypeptides of the invention
XX
SQ Sequence 1153 AA;

Query Match 100.0%; Score 966; DB 5; Length 1153;
Best Local Similarity 99.5%; Pred. No. 2.5e-96;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKKSKTLFSLMQYSEFRHFHFK 60
DB 144 CPQEDSIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKKSKTLFSLMQYSEFRHFHFK 203

QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 263

QY 121 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323

QY 181 IQNQLREKX 189
DB 324 IQNQLREKI 332

RESULT 7
ID ABG61469 standard; protein; 1153 AA.
XX
AC ABG61469;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human Beta2 integrin alphaCD11b subunit.
XX
KW Beta2 integrin; alphaD subunit; CD11c subunit; CD11b subunit; LAD;
KW leukocyte adhesion deficiency; inflammatory response; diabetes;
KW multiple sclerosis; arthritis; graft atherosclerosis; neuroprotective;
KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW immune complex alveolitis; leukaemia; ICAM-R; VCAM-1; anti-inflammatory;
KW intracellular cell adhesion molecule; vascular cell adhesion molecule;
KW locomotor recovery; locomotor damage; locomotor impairment;
KW autonomic dysfunction; sensory dysfunction; spinal cord injury.
XX
OS Homo sapiens.
XX
PN WO200230980-A2.
XX
PD 18-APR-2002.
XX
PF 15-OCT-2001; 2001WO-US032059.
XX
PR 13-OCT-2000; 2000US-00688307.
XX
PA (ICOS-) ICOS CORP.
XX
PI Gallatin WM, Van Der Vieren M;
XX
DR WPI; 2002-463260/49.
XX
PT Use of an anti-alpha-d monoclonal antibodies for promoting locomotor
PT recovery, inhibiting locomotor damage, limiting locomotor impairment, or
PT limiting autonomic and sensory dysfunction following spinal cord injury.
XX
PS Example 5; Page 191-194; 270pp; English.

XX The invention relates to promoting locomotor recovery, inhibiting
CC locomotor damage, limiting locomotor impairment, or limiting autonomic
CC and sensory dysfunction following spinal cord injury by administering an
CC anti-alpha d (Beta2 integrin alpha2 subunit) monoclonal antibody to a
CC spinal cord injury victim. The method also involves the use of a ligand
CC selected from ICAM-R or VCAM-1 (intracellular cell adhesion molecule,
CC vascular cell adhesion molecule). The method is useful for promoting
CC locomotor recovery, inhibiting locomotor damage, limiting locomotor
CC impairment, or limiting autonomic and sensory dysfunction following
CC spinal cord injury. In particular, the spinal cord injury comprises
CC compression of the spinal cord. The antibodies are also useful for
CC reducing inflammation at the site of a central nervous system injury. The
CC specification also details the identification of Beta2 integrin alphaD
CC CDNAs and proteins, for use in raising the antibodies. Beta2 integrins
CC are implicated in diseases such as LAD (leukocyte adhesion deficiency,
CC inflammatory response, diabetes, multiple sclerosis, arthritis, graft
CC atherosclerosis, inflammatory bowel disease, Crohn's disease, ulcerative
CC colitis, immune complex alveolitis and leukaemia. The present sequence is
CC a Beta2 integrin alpha subunit sequence included for comparison with the
CC Beta2 integrin alphaD protein sequences
XX
SQ Sequence 1153 AA;

Query Match 100.0%; Score 966; DB 5; Length 1153;
Best Local Similarity 99.5%; Pred. No. 2.5e-96;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKKSKTLFSLMQYSEFRHFHFK 60
DB 144 CPQEDSIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKKSKTLFSLMQYSEFRHFHFK 203

QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 263

QY 121 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323

QY 181 IQNQLREKX 189
DB 324 IQNQLREKI 332

RESULT 8
ID AA014428 standard; protein; 1153 AA.
XX
AC AA014428;
XX
DT 03-MAY-2002 (first entry)
XX
DE Integrin Mac-1 alpha subunit.
XX
KW Mac-1; integrin alpha subunit; variant integrin inserted domain protein;
KW open conformation; integrin related inflammatory disorder;
KW integrin related immunological disorder; rheumatoid arthritis; ischaemia;
KW reperfusion; hypovolemic shock; infarction; cerebral shock;
KW viral infection; cancer; gene therapy; vaccine;
KW bioactive agent screening.
XX
OS Unidentified.
XX
PN WO200204521-A2.
XX
PD 17-JAN-2002.
XX
PF 09-JUL-2001; 2001WO-US021805.
XX
PR 07-JUL-2000; 2000US-0216600P.
XX
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.


```
QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
Db 204 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGVEDVTPADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
Db 264 DPLGVEDVTPADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
QY 181 IQNQLREXK 189
Db 324 IQNQLREKI 332

RESULT 10
AAU21991
ID AAU21991 standard; protein; 187 AA.
AC AAU21991;
XX
DT 13-SEP-1999 (first entry)
DE Human complement factor MAC-1 vWF domain sequence.
XX
KW Factor B analogue; modified; complement activity; complement factor B;
KW short consensus repeat domain; von Willebrand factor domain; human; C2;
KW CR3; autoimmune response; tissue damage; lupus erythematosus; therapy;
KW rheumatoid arthritis; hemolytic anemia; myasthenia gravis; injury; MAC-1;
KW myocardial infarction; acute shock lung syndrome; inflammation; vWF.
OS Homo sapiens.
XX
PN US928892-A.
PD 27-JUL-1999.
PF 26-JUL-1996; 96US-00687706.
XX
PR 03-JAN-1994; 94US-00177109.
XX
PA (UNIW ) UNIV WASHINGTON.
PI Oglesby TJ, Hourcade DE;
XX
DR WPI; 1999-429498/36.
XX
PT Nucleic acids encoding complement protein homologues useful for
PT modulating function of the complement system in the treatment of a
XX variety of immune and autoimmune complex mediated syndromes.
PS Disclosure; Fig 5A-B; 53pp; English.
XX
CC The invention relates to a Factor B analogue that exhibits modified
CC complement activity in vitro. The analogue is generated by substituting a
CC short consensus repeat domain (SCR) or a von Willebrand Factor domain
CC (vWF) of human factor B with a SCR or a vWF from a second protein such as
CC human C2 or CR3. The analogues may be used to regulate the complement
CC system involved in immune and autoimmune responses. Complement activity
CC can account for substantial tissue damage in a wide variety of autoimmune
CC /immune complex mediated syndromes such as lupus erythematosus,
CC rheumatoid arthritis, hemolytic anemias and myasthenia gravis. Inhibition
CC of the complement system using the analogues is likely to provide a means
CC of therapeutic intervention in these cases. Inhibition of complement may
CC also be favorable in cases that involve tissue damage caused by vascular
CC injury such as myocardial infarction, cerebral vascular accidents or
CC acute shock lung syndrome. In these cases the complement system may
CC contribute to the destruction of partially damaged tissue as in
CC reperfusion injury. In addition, the use of complement analogues with
CC novel target specificities could reduce the activity of tissue damaging
CC proteins at sites of inflammation. Complement inhibition is important in
CC the prevention of xenograft rejection (the inhibition of complement by
CC cell-associated and soluble inhibitors is useful in protecting the
CC transplant from damage caused by activation of endogenous complement. The
CC present sequence represents the vWF domain of human factor MAC-1
```

```
XX SQ Sequence 187 AA;
Query Match 99.4%; Score 960; DB 2; Length 187;
Best Local Similarity 100.0%; Pred. No. 8.9e-97;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CPQEDSDIAFLIDGSGSIIPHDFFRMKEFVSTVMBQLKKSKTLFSLMQYSEEFRIHFTFK 60
Db 1 CPQEDSDIAFLIDGSGSIIPHDFFRMKEFVSTVMBQLKKSKTLFSLMQYSEEFRIHFTFK 60
QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
Db 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
QY 121 DPLGVEDVTPADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
Db 121 DPLGVEDVTPADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
QY 181 IQNQLRE 187
Db 181 IQNQLRE 187

RESULT 11
AAU76856
ID AAU76856 standard; protein; 191 AA.
XX
AC AAU76856;
XX
DT 21-MAY-2002 (first entry)
DE Human integrin alpha subunit CD11b variant A domain.
XX
KW Human; integrin alpha subunit; A domain; CD11b; integrin beta subunit;
KW A-like domain; inflammatory disorder; skeletal muscle injury; retinosis;
KW ischaemia-reperfusion injury; immune complex; parasitic disease; mutant;
KW antiinflammatory; vasotropic; antiparasitic; vulnerary; gene therapy;
KW mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 189 /label= Gly, Ala
FT /note= "Wild-type Ile substituted by Gly or Ala"
XX
PN WO200209737-A1.
XX
PD 07-FEB-2002.
XX
PF 31-JUL-2001; 2001WO-US023957.
XX
PR 31-JUL-2000; 2000US-0221950P.
PR 11-JAN-2001; 2001US-00758493.
PR 13-MAR-2001; 2001US-00805354.
XX
PA (GEO ) GEN HOSPITAL CORP.
XX
PI Arnaout AM, Li R, Xiong J;
XX
DR WPI; 2002-188687/24.
XX
PT Novel high affinity integrin polypeptide useful for treating restenosis
PT and parasitic diseases, comprises all or part of variant integrin alpha
PT subunit A domain or variant integrin beta subunit A-like domain.
PS Claim 2; Page; 55pp; English.
XX
CC The invention relates to a high affinity integrin polypeptide comprising
CC all or part of a variant integrin alpha subunit A domain or a variant
CC integrin beta subunit A-like domain. The polypeptide, preferably the
```

CC CD11b alpha subunit A domain, where I at residue 332 has been replaced by
CC G or A, F at residue 313 and A at residue 320 have been replaced by C, or
CC V at residue 315 and A at residue 320 have been replaced by C, is useful
CC for determining if a test compound is a candidate compound for binding to
CC CD11b or for treating an inflammatory disorder, by contacting a test
CC compound with the polypeptide and determining if the test compound binds
CC to the polypeptide. The integrin subunits are useful for reducing
CC skeletal muscle injury, for treating disorders caused by ischaemia-
CC reperfusion injury, immune complexes, restenosis and parasitic diseases,
CC to purify variant integrin polypeptide ligands and as bait proteins in
CC two-hybrid or three-hybrid assays. This sequence represents a human
CC integrin alpha subunit CD11b variant A domain. Note: This variant
CC sequence is not featured in the specification but has been derived from
CC the wild-type protein shown in AAU76847
XX
SQ Sequence 191 AA;

Query Match 99.0%; Score 956; DB 5; Length 191;
Best Local Similarity 98.4%; Pred. No. 2.5e-96;
Matches 186; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60
DB 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60
QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNTGARKNAFKLVVITDGEKFG 120
DB 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNTGARKNAFKLVVITDGEKFG 120
QY 121 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 121 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
QY 181 IQNQLREKX 189
DB 181 IQNQLREKX 189
RESULT 12
AAU76847
ID AAU76847 standard; protein; 191 AA.
AC AAU76847;
DT 21-MAY-2002 (first entry)
DE Human integrin alpha subunit CD11b A domain.
KW Human; integrin alpha subunit; A domain; CD11b; integrin beta subunit;
KW A-like domain; inflammatory disorder; skeletal muscle injury; restenosis;
KW ischaemia-reperfusion injury; immune complex; parasitic disease;
KW antiinflammatory; vasotropic; antiparasitic; vulnerary; gene therapy.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Region 1. 188
XX /note="This region is specifically claimed"
FN WO200209737-A1.
PN
XX
XX
XX 07-FEB-2002.
XX
XX 31-JUL-2001; 2001WO-US023957.
XX
XX 31-JUL-2000; 2000US-0221950P.
PR 11-JAN-2001; 2001US-00758493.
PR 13-MAR-2001; 2001US-00805354.
XX
XX (GEO) GEN HOSPITAL CORP.
XX
XX Arnaout AM, Li R, Xiong J;
XX

DR WPI; 2002-188687/24.
XX Novel high affinity integrin polypeptide useful for treating restenosis
PT and parasitic diseases, comprises all or part of variant integrin alpha
PT subunit A domain or variant integrin beta subunit A-like domain.
XX
PS Example 2; Fig 5; 55pp; English.
XX The invention relates to a high affinity integrin polypeptide comprising
CC all or part of a variant integrin alpha subunit A domain or a variant
CC integrin beta subunit A-like domain. The polypeptide, preferably the
CC CD11b alpha subunit A domain, where I at residue 332 has been replaced by
CC G or A, F at residue 313 and A at residue 320 have been replaced by C, or
CC V at residue 315 and A at residue 320 have been replaced by C, is useful
CC for determining if a test compound is a candidate compound for binding to
CC CD11b or for treating an inflammatory disorder, by contacting a test
CC compound with the polypeptide and determining if the test compound binds
CC to the polypeptide. The integrin subunits are useful for reducing
CC skeletal muscle injury, immune complexes, restenosis and parasitic diseases,
CC reperfusion injury, immune complexes, restenosis and parasitic diseases,
CC to purify variant integrin polypeptide ligands and as bait proteins in
CC two-hybrid or three-hybrid assays. This sequence represents the human
CC integrin alpha subunit CD11b A domain
XX
SQ Sequence 191 AA;
Query Match 99.0%; Score 956; DB 5; Length 191;
Best Local Similarity 97.9%; Pred. No. 2.5e-96;
Matches 185; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60
DB 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60
QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNTGARKNAFKLVVITDGEKFG 120
DB 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNTGARKNAFKLVVITDGEKFG 120
QY 121 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 121 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
QY 181 IQNQLREKX 189
DB 181 IQNQLREKX 189
RESULT 13
AAB66766
ID AAB66766 standard; protein; 216 AA.
XX
AC AAB66766;
XX
DT 10-APR-2001 (first entry)
DE Amino acids 149-353 of human CR-3 alpha chain and His tag.
XX
XX EST; expressed sequence tag; inclusion body; binding partner;
KW immunoglobulins.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200102588-A2.
XX
XX 11-JAN-2001.
PD
XX 30-JUN-2000; 2000WO-EP006137.
PF
XX 02-JUL-1999; 99EP-00112815.
PR
XX (MORP-) MORPHOSYS AG.
PA
XX

PI Frisch C, Kretschmar T, Hoess A, Von Rueden T;
XX WPI; 2001-147085/15.
XX
XX Generating specific binding partners to (poly)peptides encoded by genomic
PT DNA fragments, involves forming inclusion bodies by expressing the
PT (poly)peptide as part of fusion proteins.
XX
XX Disclosure; Page 18; 45pp; English.
XX
XX The present invention relates to generating a specific binding partner to
CC a peptide, encoded by a genomic DNA fragment or an expressed sequence tag
CC (EST). A nucleic acid molecule encoding a fusion protein is expressed in
CC a host cell to allow the formation of inclusion bodies comprising the
CC fusion protein, the inclusion bodies are isolated and a specific binding
CC partner is generated. The specific binding partners generated are useful
CC for identifying and characterizing naturally occurring proteins e.g. as
CC immunoglobulins or fragments in immunoassays
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SQ Sequence 216 AA;
Query Match 96.7%; Score 934; DB 4; Length 216;
Best Local Similarity 99.5%; Pred. No. 7.8e-94;
Matches 183; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 6 SDIAFLIDGSGSIIPHDPRMKEFVSTVMEQKKSKTLFSLMQYSEEPRIHFTFKFQNN 65
DB 12 SDIAFLIDGSGSIIPHDPRMKEFVSTVMEQKKSKTLFSLMQYSEEPRIHFTFKFQNN 71
QY 66 PNPRSLVKPITQLGRTHTATGIRKVVRELFNTNGARKNAFKILVITDGGKFGDPLGY 125
DB 72 PNPRSLVKPITQLGRTHTATGIRKVVRELFNTNGARKNAFKILVITDGGKFGDPLGY 131
QY 126 EDVPEADREGVIRYVIGVDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKTIQNOL 185
DB 132 EDVPEADREGVIRYVIGVDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKTIQNOL 191
QY 186 REKX 189
DB 192 REKI 195
RESULT 14
AAR77461
ID AAR77461 standard; peptide; 435 AA.
AC AAR77461;
XX
XX 27-AUG-2003 (revised)
DT 12-FEB-1996 (first entry)
XX
XX GST-I-domain fusion protein.
DE
XX Leukocyte beta-2-integrin Mac-1; I-domain; CD11b; fusion protein;
KW glutathione-S-transferase; GST; Factor-Xa; antiinflammatory.
XX
XX Unidentified.
OS
XX Homo sapiens.
OS
XX Chimeric.
OS
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Protein 1..221
FT /label= GST
FT Peptide 222..228
FT /label= Factor-Xa recognition_sequence
FT Cleavage-site 225..226
FT Peptide 229..230
FT /label= Spacer
FT /note= "spacer allows accommodation of Factor-Xa at the
FT cleavage site"
FT 231..435
FT Protein
FT /label= I-domain

XX WO9529243-A1.
FN
XX
XX 02-NOV-1995.
PD
XX
XX 19-APR-1995; 95WO-US004439.
PF
XX
XX 26-APR-1994; 94US-00233596.
PR
XX
XX (UPJO) UPJOHN CO.
PA
XX
XX Heinrichson RL, Anderson DC, Tomich CC, Fairbanks MB;
PI Bajt-Jaeschke ML;
PI
XX
XX WPI; 1995-382991/49.
DR
XX
XX Glutathione-S-transferase fusion protein with Factor Xa cleavage site -
PT for prodn. of I-domain from leukocyte B2-integrin Mac-1.
PT
XX
XX Claim 1; Page 32-34; 41pp; English.
PS
XX
XX A fusion protein comprises a glutathione-S-transferase fusion partner,
CC used to increase the level of soluble protein expression in E. coli and
CC to facilitate affinity purification, and the human leukocyte beta-2-
CC integrin Mac-1 I-domain, linked by a Factor-Xa recognition sequence that
CC allows cleavage of the fusion protein and recovery of the I-domain, which
CC is useful as an antiinflammatory. (Updated on 27-AUG-2003 to correct OS
CC field.)
CC
XX
SQ Sequence 435 AA;
Query Match 96.7%; Score 934; DB 2; Length 435;
Best Local Similarity 99.5%; Pred. No. 2.1e-93;
Matches 183; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 6 SDIAFLIDGSGSIIPHDPRMKEFVSTVMEQKKSKTLFSLMQYSEEPRIHFTFKFQNN 65
DB 231 SDIAFLIDGSGSIIPHDPRMKEFVSTVMEQKKSKTLFSLMQYSEEPRIHFTFKFQNN 290
QY 66 PNPRSLVKPITQLGRTHTATGIRKVVRELFNTNGARKNAFKILVITDGGKFGDPLGY 125
DB 291 PNPRSLVKPITQLGRTHTATGIRKVVRELFNTNGARKNAFKILVITDGGKFGDPLGY 350
QY 126 EDVPEADREGVIRYVIGVDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKTIQNOL 185
DB 351 EDVPEADREGVIRYVIGVDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKTIQNOL 410
QY 186 REKX 189
DB 411 REKI 414
RESULT 15
AAU76866
ID AAU76866 standard; protein; 177 AA.
XX
XX AAU76866;
AC
XX
XX 21-MAY-2002 (first entry)
DT
XX
XX Human integrin alpha subunit CD11b deletion variant A domain #2.
DE
XX
XX Human; integrin alpha subunit; A domain; CD11b; integrin beta subunit;
KW A-like domain; inflammatory disorder; skeletal muscle injury; reestenosis;
KW ischaemia-reperfusion injury; immune complex; parasitic disease; mutant;
KW antiinflammatory; vasotropic; antiparasitic; vulnerable; gene therapy;
KW mutein.
XX
XX Homo sapiens.
OS
XX Synthetic.
OS
XX Key Location/Qualifiers
FH Key
FT Misc-difference 172

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.
OM protein - protein search, using sw model
Run on: January 13, 2005, 15:13:36 ; Search time 31.2304 Seconds
(without alignments)
2186.449 Million cell updates/sec

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Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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 - 2: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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 - 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
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 - 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
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 - 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
 - 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	966	100.0	191	10	US-09-805-354-1
2	966	100.0	191	11	US-09-758-493-1
3	966	100.0	191	14	US-10-144-259-1
4	966	100.0	1152	9	US-09-945-265-4
5	966	100.0	1153	9	US-09-350-259-3
6	966	100.0	1153	10	US-09-902-481A-1
7	966	100.0	1153	14	US-09-891-943-3
8	966	100.0	1153	14	US-10-144-259-30
9	966	100.0	1153	14	US-10-207-655-176
10	957	99.1	1137	10	US-09-902-481A-6
11	951	98.4	1137	10	US-09-902-481A-5
12	941	97.4	1137	10	US-09-902-481A-4
13	940	97.3	1187	15	US-10-346-863-37

14	940	97.3	187	16	US-10-615-515-9	Sequence 9, Appli
15	939	97.2	184	15	US-10-346-863-17	Sequence 17, Appl
16	934	96.7	190	15	US-10-346-863-42	Sequence 42, Appl
17	934	96.7	190	15	US-10-346-863-48	Sequence 48, Appl
18	934	96.7	216	10	US-09-795-872-5	Sequence 5, Appli
19	934	96.7	216	16	US-10-662-824-5	Sequence 3, Appli
20	928	96.1	1137	10	US-09-902-481A-3	Sequence 11, Appl
21	737	76.3	199	14	US-10-066-551-11	Sequence 11, Appl
22	737	76.3	199	17	US-10-665-990A-11	Sequence 11, Appl
23	595	61.6	1151	9	US-09-350-259-37	Sequence 37, Appl
24	595	61.6	1151	10	US-09-891-943-37	Sequence 37, Appl
25	595	61.6	1161	9	US-09-350-259-55	Sequence 55, Appl
26	595	61.6	1161	10	US-09-891-943-55	Sequence 55, Appl
27	594	61.5	413	9	US-09-350-259-101	Sequence 101, App
28	594	61.5	413	10	US-09-891-943-101	Sequence 101, App
29	586	60.7	191	10	US-09-805-354-3	Sequence 3, Appli
30	586	60.7	191	11	US-09-758-493-3	Sequence 3, Appli
31	586	60.7	191	14	US-10-144-259-3	Sequence 3, Appli
32	586	60.7	1155	9	US-09-350-259-46	Sequence 46, Appl
33	586	60.7	1155	10	US-09-891-943-46	Sequence 46, Appl
34	586	60.7	1161	9	US-09-350-259-2	Sequence 2, Appli
35	586	60.7	1161	9	US-09-350-259-53	Sequence 53, Appl
36	586	60.7	1161	9	US-09-350-259-99	Sequence 99, Appl
37	586	60.7	1161	10	US-09-891-943-2	Sequence 2, Appli
38	586	60.7	1161	10	US-09-891-943-53	Sequence 53, Appl
39	586	60.7	1161	10	US-09-891-943-99	Sequence 99, Appl
40	542	56.1	1163	9	US-09-350-259-4	Sequence 4, Appli
41	542	56.1	1163	10	US-09-891-943-4	Sequence 4, Appli
42	540	55.9	191	10	US-09-805-354-2	Sequence 2, Appli
43	540	55.9	191	11	US-09-758-493-2	Sequence 2, Appli
44	540	55.9	191	14	US-10-144-259-2	Sequence 2, Appli
45	540	55.9	1163	14	US-10-116-275-204	Sequence 204, App

ALIGNMENTS

RESULT 1

US-09-805-354-1
; Sequence 1, Application US/09805354
; Publication No. US20030078375A1
; GENERAL INFORMATION:
; APPLICANT: Arnaout, M. Amin
; APPLICANT: Li, Rui
; APPLICANT: Xiong, Jian-Ping
; TITLE OF INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 00786-536001
; CURRENT APPLICATION NUMBER: US/09/805,354
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 09/758,493
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/221,950
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-805-354-1

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Best Local Similarity	99.5%;	Pred. No. 1.6e-93;		
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QY	1	CPQEDSDIAFLIDGSGSIIPHDPRMKGFSVTVMQOLKKSKTLFSLMQVSEFRHFTPK	60	
Db	1	CPQEDSDIAFLIDGSGSIIPHDPRMKGFSVTVMQOLKKSKTLFSLMQVSEFRHFTPK	60	
QY	61	EFQNNPNRSLVKPITOLLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG	120	
Db	61	EFQNNPNRSLVKPITOLLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG	120	

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QY 121 DPLGYEDVPEADREGVIRYVIGVDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 121 DPLGYEDVPEADREGVIRYVIGVDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180

QY 181 IQNQLREKX 189
DB 181 IQNQLREKI 189

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; Sequence 1, Application US/09758493
; Publication No. US20040086935A1
; GENERAL INFORMATION:
; APPLICANT: Arnaout, M. Amin
; APPLICANT: Li, Rui
; APPLICANT: Xiong, Jian-Ping
; TITLE OF INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 00786-804001
; CURRENT APPLICATION NUMBER: US/09/758,493
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/221,950
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-758-493-1

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Best Local Similarity 99.5%; Pred. No. 1.6e-93;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CPOEDSDIAFLIDGSGSIIPHDFFRMKEFVSTVMEQLKSKTFLSLMQYSEEFRIHFTFK 60

QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120

QY 121 DPLGYEDVPEADREGVIRYVIGVDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 121 DPLGYEDVPEADREGVIRYVIGVDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180

QY 181 IQNQLREKX 189
DB 181 IQNQLREKI 189

RESULT 3
US-10-144-259-1
; Sequence 1, Application US/10144259
; Publication No. US20030109691A1
; GENERAL INFORMATION:
; APPLICANT: Arnaout, M. Amin
; APPLICANT: Li, Rui
; APPLICANT: Xiong, Jian-Ping
; TITLE OF INVENTION: VARIANT INTEGRIN POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 00786-548001
; CURRENT APPLICATION NUMBER: US/10/144,259
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: US 09/758,493
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/221,950
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 191
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-259-1

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Best Local Similarity 99.5%; Pred. No. 1.6e-93;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CPOEDSDIAFLIDGSGSIIPHDFFRMKEFVSTVMEQLKSKTFLSLMQYSEEFRIHFTFK 60

QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120

QY 121 DPLGYEDVPEADREGVIRYVIGVDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 121 DPLGYEDVPEADREGVIRYVIGVDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180

QY 181 IQNQLREKX 189
DB 181 IQNQLREKI 189

RESULT 4
US-09-945-265-4
; Sequence 4, Application US/09945265
; Patent No. US20020123614A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy A.
; APPLICANT: Shimaoka, Motomu
; APPLICANT: Lu, Chafen
; TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A
; TITLE OF INVENTION: DESIRED CONFORMATION AND METHODS FOR PRODUCING SAME
; FILE REFERENCE: CEN-002CP
; CURRENT APPLICATION NUMBER: US/09/945,265
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,700
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-945-265-4

Query Match 100.0%; Score 966; DB 9; Length 1152;
Best Local Similarity 99.5%; Pred. No. 1.9e-92;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPOEDSDIAFLIDGSGSIIPHDFFRMKEFVSTVMEQLKSKTFLSLMQYSEEFRIHFTFK 60
DB 144 CPOEDSDIAFLIDGSGSIIPHDFFRMKEFVSTVMEQLKSKTFLSLMQYSEEFRIHFTFK 203

QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263

QY 121 DPLGYEDVPEADREGVIRYVIGVDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGYEDVPEADREGVIRYVIGVDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323

QY 181 IQNQLREKX 189
DB 324 IQNQLREKI 332

RESULT 5
US-09-350-259-3
; Sequence 3, Application US/09350259
; Patent No. US20020062008A1
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; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. US20020062008A1el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/350,259
; CURRENT FILING DATE: 1999-07-08
; EARLIER APPLICATION NUMBER: 09/193,043
; EARLIER FILING DATE: 1998-11-16
; EARLIER APPLICATION NUMBER: 08/173,497
; EARLIER FILING DATE: 1993-12-23
; EARLIER APPLICATION NUMBER: 08/286,889
; EARLIER FILING DATE: 1994-08-05
; EARLIER APPLICATION NUMBER: 08/362,652
; EARLIER FILING DATE: 1994-12-21
; EARLIER APPLICATION NUMBER: 08/943,363
; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-350-259-3

Query Match 100.0%; Score 966; DB 9; Length 1153;
Best Local Similarity 99.5%; Pred. No. 1.9e-92;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKSKTLPFSIMQYSESEFRHFTPK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKSKTLPFSIMQYSESEFRHFTPK 203

QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263

QY 121 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323

QY 181 IQNQLREKX 189
DB 324 IQNQLREKI 332

RESULT 6
US-09-902-481A-1
; Sequence 1, Application US/09902481A
; Publication No. US2003005440A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy
; APPLICANT: Shimaoka, Motomu
; APPLICANT: Shifman, Julia
; APPLICANT: Mayo, Stephen
; TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
; FILE REFERENCE: A-70586-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/902,481A
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/216,600
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (17)..()
; OTHER INFORMATION:
US-09-902-481A-1

Query Match 100.0%; Score 966; DB 9; Length 1153;
Best Local Similarity 99.5%; Pred. No. 1.9e-92;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKSKTLPFSIMQYSESEFRHFTPK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKSKTLPFSIMQYSESEFRHFTPK 203

QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263

QY 121 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323

QY 181 IQNQLREKX 189
DB 324 IQNQLREKI 332

RESULT 7
US-09-891-943-3
; Sequence 3, Application US/09891943
; Publication No. US20030077278A1
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. US20030077278A1el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/891,943
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 09/193,043
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/286,889
; PRIOR FILING DATE: 1994-08-05
; PRIOR APPLICATION NUMBER: 08/362,652
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/943,363
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-891-943-3

Query Match 100.0%; Score 966; DB 10; Length 1153;
Best Local Similarity 99.5%; Pred. No. 1.9e-92;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKSKTLPFSIMQYSESEFRHFTPK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKSKTLPFSIMQYSESEFRHFTPK 203

QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263

QY 121 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323

QY 181 IQNQLREKX 189
DB 324 IQNQLREKI 332

RESULT 8
US-10-144-259-30
; Sequence 30, Application US/10144259
; Publication No. US20030109691A1
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; GENERAL INFORMATION:
; APPLICANT: Arnaut, M. Amin
; APPLICANT: Li, Rui
; APPLICANT: Xiong, Jian-Ping
; TITLE OF INVENTION: VARIANT INTEGRIN POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 00786-548001
; CURRENT APPLICATION NUMBER: US/10/144,259
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: US 09/758,493
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/221,950
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-259-30

Query Match      100.0%; Score 966; DB 14; Length 1153;
Best Local Similarity 99.5%; Pred. No. 1.9e-92;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 CPQEDSDIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 60
DB      144 CPQEDSDIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 203

QY      61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
DB      204 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 263

QY      121 DPLGYEDVIPADREGVIRYVIGVDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB      264 DPLGYEDVIPADREGVIRYVIGVDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323

QY      181 IQNQLREKX 189
DB      324 IQNQLREKI 332

RESULT 9
US-10-207-655-176
; Sequence 176, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 176
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-176

Query Match      100.0%; Score 966; DB 14; Length 1153;
Best Local Similarity 99.5%; Pred. No. 1.9e-92;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 CPQEDSDIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 60
DB      144 CPQEDSDIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 203

QY      61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
DB      204 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 263

QY      121 DPLGYEDVIPADREGVIRYVIGVDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB      264 DPLGYEDVIPADREGVIRYVIGVDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
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DB      264 DPLGYEDVIPADREGVIRYVIGVDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323

QY      181 IQNQLREKX 189
DB      324 IQNQLREKI 332

RESULT 10
US-09-902-481A-6
; Sequence 6, Application US/09902481A
; Publication No. US20030054440A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy
; APPLICANT: Shimaoka, Motomu
; APPLICANT: Shifman, Julia
; APPLICANT: Mayo, Stephen
; TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
; FILE REFERENCE: A-70586-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/902,481A
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/216,600
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 1137
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-902-481A-6

Query Match      99.1%; Score 957; DB 10; Length 1137;
Best Local Similarity 97.4%; Pred. No. 1.7e-91;
Matches 184; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      1 CPQEDSDIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 60
DB      128 CPQEDSDIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 187

QY      61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
DB      188 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 247

QY      121 DPLGYEDVIPADREGVIRYVIGVDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB      248 DPLGYEDVIPADREGVIRYVIGVDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 307

QY      181 IQNQLREKX 189
DB      308 IQNQLREKI 316

RESULT 11
US-09-902-481A-5
; Sequence 5, Application US/09902481A
; Publication No. US20030054440A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy
; APPLICANT: Shimaoka, Motomu
; APPLICANT: Shifman, Julia
; APPLICANT: Mayo, Stephen
; TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
; FILE REFERENCE: A-70586-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/902,481A
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/216,600
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1137
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TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic
US-09-902-481A-5

Query Match 98.4%; Score 951; DB 10; Length 1137;
Best Local Similarity 95.2%; Pred. No. 7.1e-91;
Matches 180; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 60
DB 128 CPQEDSIAFLVDGSGSIIPHDPRAKEFISTVMEQLKSKTLFSLMOYSEEFRIHFTFK 187

QY 61 EFQNNPNRSLVKPITQLGRTHHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 188 EFQNNPNRSLIKPITQLGRTHHTATGIRKVVRELFNITNGARKNAFKILITDGEKFG 247

QY 121 DPLGYEDVIPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 248 DPLGYEDVIPEADREGVIRYVIGVDAPRSEKSRQELNTVASKPPRDHVFQINNFEALKT 307

QY 181 IQNQLREKX 189
DB 308 IQNQLREKI 316

RESULT 12
US-09-902-481A-4
Sequence 4, Application US/09902481A
Publication No. US2003005440A1
GENERAL INFORMATION:
APPLICANT: Springer, Timothy
APPLICANT: Shimaoka, Motomu
APPLICANT: Shifman, Julia
APPLICANT: Mayo, Stephen
TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
FILE REFERENCE: A-70586-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/902,481A
CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/216,600
PRIOR FILING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent in version 3.1
SEQ ID NO 4
LENGTH: 1137
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic
US-09-902-481A-4

Query Match 97.4%; Score 941; DB 10; Length 1137;
Best Local Similarity 94.7%; Pred. No. 8.1e-90;
Matches 179; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

QY 1 CPQEDSIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 60
DB 128 CPQEDSIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 187

QY 61 EFQNNPNRSLVKPITQLGRTHHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 188 EFQNNPNRSLIKPITQLGRTHHTATGLRKVVRELFNITNGARKNAFKILITDGEKFG 247

QY 121 DPLGYEDVIPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 248 DPLGYEDVIPEADREGVIRYVIGVDAPRSEKSRQELNTVASKPPRDHVFQINNFEALKT 307

QY 181 IQNQLREKX 189
DB 308 IQNQLREKI 316

RESULT 13
US-10-346-863-37
Sequence 37, Application US/10346863
Publication No. US20040038325A1
GENERAL INFORMATION:
APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
APPLICANT: FAGAN, RICHARD JOSEPH
APPLICANT: GUTTERIDGE, ALEX
TITLE OF INVENTION: ADHESION MOLECULES
FILE REFERENCE: 674575-2001
CURRENT APPLICATION NUMBER: US/10/346,863
CURRENT FILING DATE: 2003-01-17
PRIOR APPLICATION NUMBER: PCT/GB01/03318
PRIOR FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: GB 0018126.3
PRIOR FILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: GB 0025447.4
PRIOR FILING DATE: 2000-10-17
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 37
LENGTH: 187
TYPE: PRT
ORGANISM: Homo sapiens
US-10-346-863-37

Query Match 97.3%; Score 940; DB 15; Length 187;
Best Local Similarity 99.5%; Pred. No. 8.5e-91;
Matches 184; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 DSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 64
DB 1 DSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 60

QY 65 NPNRSLVKPITQLGRTHHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLG 124
DB 61 NPNRSLVKPITQLGRTHHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLG 120

QY 125 YEDVIPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 184
DB 121 YEDVIPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180

QY 185 LREKX 189
DB 181 LREKI 185

RESULT 14
US-10-615-515-9
Sequence 9, Application US/10615515
Publication No. US20040132974A1
GENERAL INFORMATION:
APPLICANT: FAGAN, RICHARD JOSEPH
APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
APPLICANT: GUTTERIDGE, ALEX
TITLE OF INVENTION: ADHESION MOLECULES
FILE REFERENCE: 674575-2004
CURRENT APPLICATION NUMBER: US/10/615,515
CURRENT FILING DATE: 2003-07-08
PRIOR APPLICATION NUMBER: PCT/GB02/00107
PRIOR FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: GB 0100750.9
PRIOR FILING DATE: 2001-01-11
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patent in Ver. 3.2
SEQ ID NO 9
LENGTH: 187
TYPE: PRT
ORGANISM: Homo sapiens
US-10-615-515-9

Query Match 97.3%; Score 940; DB 16; Length 187;
Best Local Similarity 99.5%; Pred. No. 8.5e-91;

Matches 184; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 DSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTFKFQN 64
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Db 1 DSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTFKFQN 60
|||||

QY 65 NNPRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLG 124
|||||
Db 61 NNPRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLG 120
|||||

QY 125 YEDVIPEADREGVIRYVIGVDAPFSEKSRQELNTIASKPPRDHVFQVNNFEALKTIONQ 184
|||||
Db 121 YEDVIPEADREGVIRYVIGVDAPFSEKSRQELNTIASKPPRDHVFQVNNFEALKTIONQ 180
|||||

QY 185 LREKX 189
|||||
Db 181 LREKI 185
|||||

RESULT 15
US-10-346-863-17
; Sequence 17, Application US/10346863
; Publication No. US20040038325A1
; GENERAL INFORMATION:
; APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
; APPLICANT: FAGAN, RICHARD JOSEPH
; APPLICANT: GUTTERIDGE, ALEX
; TITLE OF INVENTION: ADHESION MOLECULES
; FILE REFERENCE: 674575-2001
; CURRENT APPLICATION NUMBER: US/10/346,863
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: PCT/GB01/03318
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: GB 0018126.3
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: GB 0025447.4
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-346-863-17

Query Match 97.2%; Score 939; DB 15; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-90;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTFKFQN 64
|||||
Db 1 DSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTFKFQN 60
|||||

QY 65 NNPRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLG 124
|||||
Db 61 NNPRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLG 120
|||||

QY 125 YEDVIPEADREGVIRYVIGVDAPFSEKSRQELNTIASKPPRDHVFQVNNFEALKTIONQ 184
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Db 121 YEDVIPEADREGVIRYVIGVDAPFSEKSRQELNTIASKPPRDHVFQVNNFEALKTIONQ 180
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QY 185 LREK 188
|||||
Db 181 LREK 184
|||||

Search completed: January 13, 2005, 15:39:44
Job time : 32.2304 secs

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OM protein - protein search, using sw model

Run on: January 13, 2005, 15:07:42 ; Search time 9.08295 Seconds
(without alignments)
1379.959 Million cell updates/sec

Title: RWHULB-B_COPY_144_332
Perfect score: 966
Sequence: 1 CPQEDSDIAFLIDSGSIIP.....FQVNFALKTIQNQLREKX 189

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	966	100.0	1152	2	US-08-476-062A-43
2	966	100.0	1152	5	PCT-US96-01314-43
3	966	100.0	1152	6	5424399-2
4	966	100.0	1153	1	US-08-173-497-3
5	966	100.0	1153	1	US-08-286-889-3
6	966	100.0	1153	1	US-08-485-618-3
7	966	100.0	1153	1	US-08-362-652-3
8	966	100.0	1153	2	US-08-605-672-3
9	966	100.0	1153	2	US-08-482-293A-3
10	966	100.0	1153	2	US-08-943-363-3
11	966	100.0	1153	3	US-09-193-043-3
12	966	100.0	1153	4	US-09-688-307A-3
13	966	100.0	1153	4	US-09-350-259-3
14	960	99.4	187	2	US-08-177-109A-61
15	960	99.4	187	2	US-08-687-706-61
16	934	96.7	216	4	US-09-795-872-5
17	934	96.7	435	5	PCT-US95-04439-1
18	595	61.6	1151	1	US-08-286-889-37
19	595	61.6	1151	1	US-08-485-618-37
20	595	61.6	1151	1	US-08-362-652-37
21	595	61.6	1151	2	US-08-605-672-37
22	595	61.6	1151	2	US-08-482-293A-37
23	595	61.6	1151	2	US-08-943-363-37
24	595	61.6	1151	3	US-09-193-043-37
25	595	61.6	1151	4	US-09-688-307A-37
26	595	61.6	1151	4	US-09-350-259-37
27	595	61.6	1161	1	US-08-485-618-55

28	595	61.6	1161	1	US-08-362-652-55	Sequence 55, Appl
29	595	61.6	1161	2	US-08-605-672-55	Sequence 55, Appl
30	595	61.6	1161	2	US-08-482-293A-55	Sequence 55, Appl
31	595	61.6	1161	2	US-08-943-363-55	Sequence 55, Appl
32	595	61.6	1161	3	US-09-193-043-55	Sequence 55, Appl
33	595	61.6	1161	4	US-09-688-307A-55	Sequence 55, Appl
34	595	61.6	1161	4	US-09-350-259-55	Sequence 55, Appl
35	594	61.5	413	1	US-08-485-618-101	Sequence 101, App
36	594	61.5	413	2	US-08-605-672-101	Sequence 101, App
37	594	61.5	413	2	US-08-482-293A-101	Sequence 101, App
38	594	61.5	413	2	US-08-943-363-101	Sequence 101, App
39	594	61.5	413	3	US-09-193-043-101	Sequence 101, App
40	594	61.5	413	4	US-09-688-307A-101	Sequence 101, App
41	594	61.5	413	4	US-09-350-259-101	Sequence 101, App
42	586	60.7	1155	1	US-08-286-889-46	Sequence 46, Appl
43	586	60.7	1155	1	US-08-485-618-46	Sequence 46, Appl
44	586	60.7	1155	1	US-08-362-652-46	Sequence 46, Appl
45	586	60.7	1155	2	US-08-605-672-46	Sequence 46, Appl

ALIGNMENTS

RESULT 1
US-08-476-062A-43
; Sequence 43, Application US/08476062A
; Patent No. 5877275
; GENERAL INFORMATION:
; APPLICANT: Attnout, M. Amin
; TITLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,062A
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/216,081
; FILING DATE: 21-MAR-1994
; APPLICATION NUMBER: 07/637,830
; FILING DATE: 04-JAN-1991
; APPLICATION NUMBER: 07/539,842
; FILING DATE: 18-JUN-1990
; APPLICATION NUMBER: 07/212,573
; FILING DATE: 28-JUN-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00786/068003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1152 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal

US-08-476-062A-43

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Query Match      100.0%; Score 966; DB 2; Length 1152;
Best Local Similarity 99.5%; Pred. No. 5.2e-93;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 203

QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263

QY 121 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323

QY 181 IQNQLREKX 189
DB 324 IQNQLREKI 332

RESULT 2
PCT-US96-01314-43
; Sequence 43, Application PC/TUS9601314
; GENERAL INFORMATION:
; APPLICANT: M. Amin Arnaout
; TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
; TITLE OF INVENTION: ANTAGONISTS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/01314
; FILING DATE: 30-JAN-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/380,167
; FILING DATE: 30-JAN-95
; ATTORNEY/AGENT INFORMATION:
; NAME: John W. Freeman
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00786/267001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; LENGTH: 1152
; STRANDEDNESS:
; TOPOLOGY: linear
PCT-US96-01314-43

Query Match      100.0%; Score 966; DB 5; Length 1152;
Best Local Similarity 99.5%; Pred. No. 5.2e-93;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 203

QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
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DB 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
QY 181 IQNQLREKX 189
DB 324 IQNQLREKI 332

RESULT 3
5424399-2
; Patent No. 5424399
; APPLICANT: ARNAOUT, M. AMIN
; TITLE OF INVENTION: HUMAN CR3a/b HETERODIMERS
; NUMBER OF SEQUENCES: 12
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/78,871
; FILING DATE: 16-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 539,842
; FILING DATE: 18-JUN-1990
; APPLICATION NUMBER: 212,573
; FILING DATE: 28-JUN-1988
; SEQ ID NO: 2:
; LENGTH: 1152
5424399-2

Query Match      100.0%; Score 966; DB 6; Length 1152;
Best Local Similarity 99.5%; Pred. No. 5.2e-93;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 203

QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263

QY 121 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323

QY 181 IQNQLREKX 189
DB 324 IQNQLREKI 332

RESULT 4
US-08-173-497-3
; Sequence 3, Application US/08173497
; Patent No. 5437958
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van Der Vieren, Monica
; TITLE OF INVENTION: No. 5437958el Human 2 Integrin Alpha
; TITLE OF INVENTION: Subunit
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 S. Wacker Drive, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
```

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; APPLICATION NUMBER: US/08/173,497
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5437958and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/31363
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1153 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-173-497-3

Query Match 100.0%; Score 966; DB 1; Length 1153;
Best Local Similarity 99.5%; Pred. No. 5.2e-93;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDPRMKFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
QY 181 IQNQLREXK 189
DB 324 IQNQLREXI 332

RESULT 5
US-08-286-889-3
; Sequence 3, Application US/08286889
; Patent No. 5470953
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Mich
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,889
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: P38,659
; REFERENCE/DOCKET NUMBER: 27866/32168
```

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1153 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-286-889-3

Query Match 100.0%; Score 966; DB 1; Length 1153;
Best Local Similarity 99.5%; Pred. No. 5.2e-93;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDPRMKFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
QY 181 IQNQLREXK 189
DB 324 IQNQLREXI 332

RESULT 6
US-08-485-618-3
; Sequence 3, Application US/08485618
; Patent No. 5728533
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,618
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32797
; TELECOMMUNICATION INFORMATION:
```

; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1153 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-485-618-3

Query Match 100.0%; Score 966; DB 1; Length 1153;
Best Local Similarity 99.5%; Pred. No. 5.2e-93;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQESDIAFLIDSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 60
Db 144 CPQESDIAFLIDSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPTITQLLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 120
Db 204 EFQNNPNRSLVKPTITQLLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
Db 264 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
QY 181 IQNQLREKX 189
Db 324 IQNQLREKI 332

RESULT 7

US-08-362-652-3
; Sequence 3, Application US/08362652
; Patent No. 5766850

; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/362,652
; FILING DATE:

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; ATTORNEY/AGENT INFORMATION:

; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32391
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 1153 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-362-652-3

Query Match 100.0%; Score 966; DB 1; Length 1153;
Best Local Similarity 99.5%; Pred. No. 5.2e-93;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQESDIAFLIDSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 60
Db 144 CPQESDIAFLIDSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPTITQLLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 120
Db 204 EFQNNPNRSLVKPTITQLLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
Db 264 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
QY 181 IQNQLREKX 189
Db 324 IQNQLREKI 332

RESULT 8

US-08-605-672-3
; Sequence 3, Application US/08605672
; Patent No. 5817515

; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/605,672
; FILING DATE:

; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:

; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32684
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

LENGTH: 1153 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-605-672-3

Query Match 100.0%; Score 966; DB 2; Length 1153;
Best Local Similarity 99.5%; Pred. No. 5.2e-93;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHPTFK 60
DB 144 CPQEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHPTFK 203
QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
QY 181 IQNQLREKX 189
DB 324 IQNQLREKI 332

RESULT 9

US-08-482-293A-3
Sequence 3, Application US/08482293A
Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
FILING DATE:

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-293A-3

Query Match 100.0%; Score 966; DB 2; Length 1153;
Best Local Similarity 99.5%; Pred. No. 5.2e-93;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHPTFK 60
DB 144 CPQEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHPTFK 203
QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
QY 181 IQNQLREKX 189
DB 324 IQNQLREKI 332

RESULT 10

US-08-943-363-3
Sequence 3, Application US/08943363
Patent No. 5837478
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
FILING DATE:

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
TYPE: amino acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-943-363-3

Query Match
Best Local Similarity 100.0%; Score 966; DB 2; Length 1153;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDPRRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPRDRHVFQVNNFEALKT 180
DB 264 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPRDRHVFQVNNFEALKT 323
QY 181 IQNQLREKX 189
DB 324 IQNQLREKI 332

RESULT 11
US-09-193-043-3
; Sequence 3, Application US/09193043
; Patent No. 6251395
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; TITLE OF INVENTION: No. 6251395el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/193,043
; CURRENT FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/173,497
; PRIOR FILING DATE: 1993-12-23
; EARLIER APPLICATION NUMBER: 08/286,889
; EARLIER FILING DATE: 1994-08-05
; EARLIER APPLICATION NUMBER: 08/362,652
; EARLIER FILING DATE: 1994-12-21
; EARLIER APPLICATION NUMBER: 08/943,363
; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-193-043-3

Query Match
Best Local Similarity 100.0%; Score 966; DB 3; Length 1153;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDPRRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPRDRHVFQVNNFEALKT 180
DB 264 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPRDRHVFQVNNFEALKT 323
QY 181 IQNQLREKX 189
DB 324 IQNQLREKI 332

US-09-193-043-3

Query Match
Best Local Similarity 100.0%; Score 966; DB 3; Length 1153;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDPRRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPRDRHVFQVNNFEALKT 180
DB 264 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPRDRHVFQVNNFEALKT 323
QY 181 IQNQLREKX 189
DB 324 IQNQLREKI 332

US-09-193-043-3
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```
RESULT 12
US-09-688-307A-3
; Sequence 3, Application US/09688307A
; Patent No. 6432404
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 6432404el Human Beta-2
; FILE REFERENCE: 27866/36646
; CURRENT APPLICATION NUMBER: US/09/688,307A
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 09/193,043
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/605,672
; PRIOR FILING DATE: 1996-02-22
; PRIOR APPLICATION NUMBER: 08/173,497
; PRIOR FILING DATE: 1993-12-23
; PRIOR APPLICATION NUMBER: 08/286,889
; PRIOR FILING DATE: 1994-08-05
; PRIOR APPLICATION NUMBER: 08/362,652
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/943,363
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-688-307A-3

Query Match
Best Local Similarity 100.0%; Score 966; DB 4; Length 1153;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDPRRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPRDRHVFQVNNFEALKT 180
DB 264 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPRDRHVFQVNNFEALKT 323
QY 181 IQNQLREKX 189
DB 324 IQNQLREKI 332

US-09-688-307A-3

Query Match
Best Local Similarity 99.5%; Pred. No. 5.2e-93;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDPRRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPRDRHVFQVNNFEALKT 180
DB 264 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPRDRHVFQVNNFEALKT 323
QY 181 IQNQLREKX 189
DB 324 IQNQLREKI 332

US-09-688-307A-3

Query Match
Best Local Similarity 100.0%; Score 966; DB 3; Length 1153;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDPRRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPRDRHVFQVNNFEALKT 180
DB 264 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPRDRHVFQVNNFEALKT 323
QY 181 IQNQLREKX 189
DB 324 IQNQLREKI 332

US-09-688-307A-3
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; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-350-259-3

Query Match
Best Local Similarity 100.0%; Score 966; DB 4; Length 1153;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEFRHFTFK 60
Db |||||
QY 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEFRHFTFK 203
Db |||||
QY 61 EFQNNPNRSLVKPITQLGRTHGTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
Db |||||
QY 204 EFQNNPNRSLVKPITQLGRTHGTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 263
Db |||||
QY 121 DPLGVEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVQVNNFEALKT 180
Db |||||
QY 264 DPLGVEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVQVNNFEALKT 323
Db |||||
QY 181 IQNQLREKX 189
Db |||||
QY 324 IQNQLREKI 332
Db |||||

RESULT 14
US-08-177-109A-61
; Sequence 61, Application US/08177109A
; Patent No. 5869615
; GENERAL INFORMATION:
; APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby
; TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/177,109A
; FILING DATE: 03-JAN-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: WU 107
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-177-109A-61

Query Match
Best Local Similarity 99.4%; Score 960; DB 2; Length 187;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEFRHFTFK 60
Db |||||
QY 1 EFQNNPNRSLVKPITQLGRTHGTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
Db |||||
QY 61 EFQNNPNRSLVKPITQLGRTHGTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
Db |||||

Query Match
Best Local Similarity 100.0%; Pred. No. 2e-93;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEFRHFTFK 60
Db |||||
QY 1 EFQNNPNRSLVKPITQLGRTHGTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
Db |||||
QY 61 EFQNNPNRSLVKPITQLGRTHGTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
Db |||||

Query Match
Best Local Similarity 99.4%; Score 960; DB 2; Length 187;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEFRHFTFK 60
Db |||||
QY 1 EFQNNPNRSLVKPITQLGRTHGTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
Db |||||
QY 61 EFQNNPNRSLVKPITQLGRTHGTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
Db |||||

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Db	61	EFQNNPRSLVKPIITOLLGRTHATGIRKVVRELFNITNGARKNAFKILVWITDGEKG	120
Qy	121	DPLGYEDVPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT	180
Db	121	DPLGYEDVPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT	180
Qy	181	IQNLRE	187
Db	181	IQNLRE	187

Search completed: January 13, 2005, 15:34:34
Job time : 10.0829 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 13, 2005, 15:03:32 ; Search time 5.12706 Seconds
(without alignments)
3321.665 Million cell updates/sec

Title: RWHLB-C_COPY_144_320

Perfect score: 922

Sequence: 1 CPQEDSDIAFLDGSIIIP.....NTIASKPRDRHVQCNFEC.177

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	903	97.9	1153	1 RWHLB	cell surface glyco
2	692	75.1	1153	2 S00551	leukocyte surface
3	486	52.7	1163	1 RWHLB	cell surface glyco
4	209	33.5	1179	2 A52213	integrin alpha-E c
5	265.5	28.8	1170	2 S03308	cell surface glyco
6	245	26.6	1163	2 I56126	lymphocyte fuction
7	227	24.6	493	2 A33809	cartilage matrix p
8	222	24.1	500	2 S66522	cartilage matrix p
9	215	23.3	496	2 A37979	cartilage matrix p
10	196.5	21.3	3051	2 S42373	hypothetical prote
11	194.5	21.1	1747	2 A45974	collagen alpha 1(X
12	194.5	21.1	1857	2 S31212	collagen alpha 1(X
13	194.5	21.1	1888	2 S78476	collagen alpha 1(X
14	192	20.8	3124	2 A40020	collagen alpha 1(X
15	186.5	20.2	1151	2 A45226	integrin alpha-1 c
16	179.5	19.5	741	2 T46488	hypothetical prote
17	176.5	19.1	272	2 A55348	integrin alpha-1 -
18	171.5	18.6	1180	2 A35854	integrin alpha-1 c
19	164	17.8	929	2 I51027	type XII collagen
20	157.5	17.1	2944	2 A54849	collagen alpha 1(V
21	151	16.4	1170	2 I45914	integrin alpha 2 s
22	150.5	16.3	3137	2 A37797	collagen alpha 3(V
23	144	15.6	1181	2 A33998	integrin alpha-2 c
24	144	15.6	3176	2 CGHU3A	collagen alpha 3(V
25	141	15.3	1178	2 S44142	VLA-2 protein homo
26	138	15.0	550	2 T23760	hypothetical prote
27	136	14.8	371	2 S32604	collagen alpha 2(V
28	134.5	14.6	712	2 A45638	immunodominant mic
29	132	14.3	2813	1 VMHU	von Willebrand fac

ALIGNMENTS

RESULT 1

RWHLB

cell surface glycoprotein CD11b precursor [validated] - human

N:Alternate names: complement receptor type 3 alpha chain; leukocyte adhesion protein Mac
eukocyte integrin alpha chain; neutrophil adherence receptor alphaM chain

C:Species: Homo sapiens (man)

C>Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text change 09-Jul-2004

C:Accession: A31108; A28915; A41600; A30892; A32218; A46526; A26091; I52567

R:Corbi, A.L.; Kishimoto, T.K.; Miller, L.J.; Springer, T.A.

J. Biol. Chem. 263, 12403-12411, 1988

A:Title: The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, CD1

B.

A:Reference number: A31108; MUID:88315033; PMID:2457584

A:Accession: A31108

A:Molecule type: mRNA

A:Residues: 1-1153 <COR>

A:Cross-references: UNIPROT:P11215; GB:J03925; NID:G187284; PIDN:AAA59544.1; PID:G307148

A>Note: part of this sequence was confirmed by protein sequencing

R:Arnaout, M.A.; Gupta, S.K.; Pierce, M.W.; Tenen, D.G.

J. Cell Biol. 106, 2153-2158, 1988

A:Title: Amino acid sequence of the alpha subunit of human leukocyte adhesion receptor M

A:Reference number: A28915; MUID:88257215; PMID:2454931

A:Accession: A28915

A:Molecule type: mRNA

A:Residues: 1-499,501-965,'P',967-1153 <ARN>

A:Cross-references: GB:M18044; GB:J03270; GB:M19664; GB:X07421; NID:G186935; PIDN:AAA594;

A>Note: the authors translated the codon TAC for residue 1129 as Thr

A>Note: part of this sequence, including the amino end of the mature protein, was confirm

R:Shelley, C.S.; Arnaout, M.A.

Proc. Natl. Acad. Sci. U.S.A. 88, 10525-10529, 1991

A:Title: The promoter of the CD11b gene directs myeloid-specific and developmentally regu

A:Reference number: A41600; MUID:92073318; PMID:1683702

A:Accession: A41600

A:Molecule type: DNA

A:Residues: 1-9 <SHE>

A:Cross-references: GB:M76724; NID:G180018; PIDN:AAA58410.1; PID:G553215

R:Arnaout, M.A.; Remold-O'Donnell, E.; Pierce, M.W.; Harris, P.; Tenen, D.G.

Proc. Natl. Acad. Sci. U.S.A. 85, 2776-2780, 1988

A:Title: Molecular cloning of the alpha-subunit of human and guinea pig leukocyte adhesic

A:Reference number: A94193; MUID:88190151; PMID:2833753

A:Accession: A30892

A:Molecule type: mRNA

A:Residues: 917-1042 <AR2>

A:Cross-references: GB:M18044

R:Hickstein, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J.

Proc. Natl. Acad. Sci. U.S.A. 86, 257-261, 1989

A:Title: cDNA sequence for the alphaM subunit of the human neutrophil adherence receptor

A:Reference number: A32218; MUID:8909893; PMID:2563162

A:Accession: A32218

A:Molecule type: mRNA

A:Residues: 9-1153 <HTC>

A:Cross-references: GB:J04145; NID:G189068; PIDN:AAA59903.1; PID:G386975

A>Note: part of this sequence was confirmed by protein sequencing
R:Fleming, J.C.; Pahl, H.L.; Gonzalez, D.A.; Smith, T.F.; Tenen, D.G.
J. Immunol. 150, 480-490, 1993
A>Title: Structural analysis of the CD11b gene and phylogenetic analysis of the alpha-in during evolution.
A:Reference number: A46526; MUID:93123748; PMID:8419480
A:Accession: A46526
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-499,501-1153 <FLE>
A:Cross-references: GB:S52227; NID:9263047; PIDN:AAE24821.1; PID:9263049
A>Note: the last three bases of intron 13, CAG, are included in some but not all mature
A>Note: sequence extracted from NCBI backbone (NCBIP:121963)
R:Pierce, M.W.; Remold-O'Donnell, E.; Todd III, R.F.; Arnaout, M.A.
Biochim. Biophys. Acta 874, 368-371, 1986
A>Title: N-terminal sequence of human leukocyte glycoprotein Mol: conservation across sp
A:Reference number: A90664; MUID:87076671; PMID:3539202
A:Accession: A26091
A:Molecule type: protein
A:Residues: 17-31 <PIE>
A:Experimental source: granulocytes
R:Pahl, H.L.; Rosmarin, A.G.; Tenen, D.G.
Blood 79, 865-870, 1992
A>Title: Characterization of the myeloid-specific CD11b promoter.
A:Reference number: I52567; MUID:92144986; PMID:1346576
A:Accession: I52567
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-9 <RES>
A:Cross-references: GB:M84477; NID:9180184; PIDN:AAA51960.1; PID:9553219
C:Comment: A common beta chain (CD18) forms a heterodimer with this chain to form Mac-1
C:Genetics:
A:Gene: GDB:ITGAM; CR3A
A:Cross-references: GDB:120599; OMIM:120980
A:Map position: 16p11.2-16p11.2
A>Note: promoter contains a GATA motif and two Sp1 consensus binding sites
C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homodimer; mag
C:Keywords: alternative splicing; calcium; cell adhesion; glycoprotein; heterodimer; mag
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-1153/Product: cell surface glycoprotein CD11b #status experimental <MAT>
F:17-1108/Domain: extracellular #status predicted <EXT>
F:148-318/Domain: von Willebrand factor type A repeat homology <VWA2>
F:465-473/Region: calcium/magnesium binding #status predicted
F:530-538/Region: calcium/magnesium binding #status predicted
F:593-601/Region: calcium/magnesium binding #status predicted
F:1109-1134/Domain: transmembrane #status predicted <TM>
F:1135-1153/Domain: intracellular #status predicted <INT>
F:86,240,391,469,693,735,802,881,901,912,941,947,979,994,1022,1045,1051,1076/Binding

Query Match 97.9%; Score 903; DB 1; Length 1153;
Best Local Similarity 99.4%; Pred. No. 5.6e-72;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CPQEDSIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKKSKTLFSLMQYSEFRIHFTFK 60
Db 144 CPQEDSIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKKSKTLFSLMQYSEFRIHFTFK 203

Qy 61 EFQNNPRLSVKPTQLGRTHATGIRKVRLEFNTNGARKNAFKILVITDGEKFG 120
Db 204 EFQNNPRLSVKPTQLGRTHATGIRKVRLEFNTNGARKNAFKILVITDGEKFG 263

Qy 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPRDRHVFCNNFE 176
Db 264 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPRDRHVFCNNFE 319

RESULT 2
RWHULC
cell surface glycoprotein CD11c precursor - human
N:Alternate names: leukocyte adhesion receptor p150,95 alpha chain
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C:Accession: A36584; A35543; S00864
R:Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A.
J. Biol. Chem. 265, 12750-12751, 1990
A:Reference number: A36584
A:Contents: erratum
A:Accession: A36584
A:Molecule type: DNA
A:Residues: 1-1163 <COR>
A:Cross-references: UNIPROT:P20702
A>Note: this revision to the sequence from reference A35543 includes the carboxyl end
R:Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A.
J. Biol. Chem. 265, 2782-2788, 1990
A>Title: Genomic structure of an integrin alpha subunit, the leukocyte p150,95 molecule.
A:Reference number: A35543; MUID:90153906; PMID:2303426
A:Accession: A35543
A:Molecule type: DNA
A:Residues: 1-834 <CO2>
A>Note: this sequence has been revised in reference A36584
R:Corbi, A.L.; Miller, L.J.; O'Connor, K.; Larson, R.S.; Springer, T.A.
EMBO J. 6, 4023-4028, 1987
A>Title: cDNA cloning and complete primary structure of the alpha subunit of a leukocyte
A:Reference number: S00864; MUID:88166645; PMID:3327687
A:Accession: S00864

R:Pytela, R.
EMBO J. 7, 1371-1378, 1988
A>Title: Amino acid sequence of the murine Mac-1 alpha chain reveals homology with the ir
A:Reference number: S00551; MUID:88312584; PMID:3044779
A:Accession: S00551
A:Molecule type: DNA
A:Residues: 1-1153 <PYT>
A:Cross-references: UNIPROT:P05555; EMBL:X07640; NID:952982; PIDN:CAA30479.1; PID:952983
A>Note: the authors translated the codon CAC for residue 569 as Gln
R:Satre, L.; Roman, J.M.; Teplow, D.B.; Dreyer, W.J.; Gee, C.E.; Larson, R.S.; Roberts,
Proc. Natl. Acad. Sci. U.S.A. 83, 5644-5648, 1986
A>Title: A partial genomic DNA clone for the alpha subunit of the mouse complement receptor
A:Reference number: I59078; MUID:86287312; PMID:2942940
A:Accession: I59078
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 11-44 <RES>
A:Cross-references: GB:M14293; NID:9198993; PIDN:AAA39484.1; PID:9554193
C:Genetics:
A:Gene: Mac-1
C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homodimer; mag
C:Keywords: cell adhesion; glycoprotein; transmembrane protein
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-1153/Product: leukocyte surface glycoprotein Mac-1 alpha chain #status experimental
F:148-318/Domain: von Willebrand factor type A repeat homology <VWA2>
F:1106-1129/Domain: transmembrane #status predicted <TM>

Query Match 75.1%; Score 692; DB 2; Length 1153;
Best Local Similarity 77.3%; Pred. No. 3e-53;
Matches 136; Conservative 18; Mismatches 22; Indels 0; Gaps 0;

Qy 1 CPQEDSIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKKSKTLFSLMQYSEFRIHFTFK 60
Db 144 CPQEDSIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKKSKTLFSLMQYSEFRIHFTFK 203

Qy 61 EFQNNPRLSVKPTQLGRTHATGIRKVRLEFNTNGARKNAFKILVITDGEKFG 120
Db 204 DFKENPRLSVKPTQLGRTHATGIRKVRLEFNTNGARKNAFKILVITDGEKFG 263

Qy 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPRDRHVFCNNFE 176
Db 264 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPRDRHVFCNNFE 319

RESULT 3
RWHULC
cell surface glycoprotein CD11c precursor - human
N:Alternate names: leukocyte adhesion receptor p150,95 alpha chain
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C:Accession: A36584; A35543; S00864
R:Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A.
J. Biol. Chem. 265, 12750-12751, 1990
A:Reference number: A36584
A:Contents: erratum
A:Accession: A36584
A:Molecule type: DNA
A:Residues: 1-1163 <COR>
A:Cross-references: UNIPROT:P20702
A>Note: this revision to the sequence from reference A35543 includes the carboxyl end
R:Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A.
J. Biol. Chem. 265, 2782-2788, 1990
A>Title: Genomic structure of an integrin alpha subunit, the leukocyte p150,95 molecule.
A:Reference number: A35543; MUID:90153906; PMID:2303426
A:Accession: A35543
A:Molecule type: DNA
A:Residues: 1-834 <CO2>
A>Note: this sequence has been revised in reference A36584
R:Corbi, A.L.; Miller, L.J.; O'Connor, K.; Larson, R.S.; Springer, T.A.
EMBO J. 6, 4023-4028, 1987
A>Title: cDNA cloning and complete primary structure of the alpha subunit of a leukocyte
A:Reference number: S00864; MUID:88166645; PMID:3327687
A:Accession: S00864

A:Molecule type: mRNA
A:Residues: 1-755, 'L', 757-1163 <CO3>
A:CROSS-references: GB:M81695; EMBL:Y00093; NID:g487829; PIDN:AAA59180.1; PID:g487830
A>Note: part of this sequence was confirmed by protein sequencing
C:Comment: A common beta chain (CD18) forms a heterodimer with CD11b to form Mac-1 on my
C:Genetics:
A:Gene: GDB:ITGAX; CD11C
A:CROSS-references: GDB:119758; OMIM:151510
A:Map position: 16p11.2-16p11.2
C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homol
C:Keywords: calcium; cell adhesion; glycoprotein; heterodimer; magnesium; tandem repeat;
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-1163/Product: cell surface glycoprotein CD11c #status predicted <MAT>
F:20-1107/Domain: extracellular #status predicted <EXT>
F:149-319/Domain: von Willebrand factor type A repeat homology <VWA4>
F:1108-1133/Domain: transmembrane #status predicted <TM>
F:1134-1163/Domain: intracellular #status predicted <INT>
F:61,89,392,697,735,899,939,1050/Binding site: carbohydrate (Asn) (covalent) #status pre

Query Match 52.7%; Score 486; DB 1; Length 1163;
Best Local Similarity 53.4%; Pred. No. 6e-35;
Matches 94; Conservative 33; Mismatches 49; Indels 0; Gaps 0;

QY 1 CPQEDSIAFLIDGSGSIIPHDFFRMKFEVSTVMEQLKKSKTLFSLMOYSEBFRHFTFK 60
DB 145 CPQEDIVFLIDGSGSISSRNFAFMNFVRAVISQFORPSTQFSLMQFSNKFQTHFTFE 204
QY 61 EFQNNPRSLVKPTQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 205 EFRRTSNPLSLASVHQLOGFTYATATQNVVHLFHASGARRATKILVITDGEKFG 264
QY 121 DPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQCNPE 176
DB 265 DSLDYKVIPMAAGIIRYAIGVGLAFONRNSWELNLIASQSEHIFKVEDFD 320

RESULT 4
A53213
Integrin alpha-E chain - human
C:Species: Homo sapiens (man)
C:Date: 19-Oct-1995 #sequence_revision 31-Mar-2001 #text_change 09-Jul-2004
C:Accession: A53213
R:Shaw, S.K.; Cepek, K.L.; Murphy, E.A.; Russell, G.J.; Brenner, M.B.; Parker, C.M.
J. Biol. Chem. 269, 6016-6025, 1994
A:Title: Molecular cloning of the human mucosal lymphocyte integrin alpha(E) subunit. Un
A:Reference number: A53213; MUID:94164962; PMID:8119947
A:Accession: A53213
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1179 <SHA>
A:CROSS-references: UNIPROT:P38570; GB:L25851; NID:g457244; PID:g457245
C:Genetics:
A:Gene: GDB:ITGAE
A:CROSS-references: GDB:330801
A:Map position: 17p13
C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homol
F:199-371/Domain: von Willebrand factor type A repeat homology <VWA3>

Query Match 33.5%; Score 309; DB 2; Length 1179;
Best Local Similarity 38.4%; Pred. No. 3.2e-19;
Matches 66; Conservative 39; Mismatches 65; Indels 2; Gaps 1;

QY 6 SDIAFLIDGSGSIIPHDFFRMKFEVSTVMEQL--KKSKTLFSLMOYSEBFRHFTFKBFQ 63
DB 201 TEAIIIDGSGSIDPDPORAKDFISNMWNFNFKCFECNFALVQGVIGVITFDLRDSQ 260
QY 64 NNPNSRLVKPTQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPL 123
DB 261 DVWASLARQNTITGVGSVTKTASAMQHVLDSIFTSHGSRKASKVMVVLTDGGIFEDPL 320
QY 124 GYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQCNPF 175
DB 321 NLTTVINSRPMQGVVERFAIGVGEFEEKSARTARELNLIASDPDETHAFKVTNY 372

RESULT 5

S03308
cell surface glycoprotein CD11a precursor - human
N:Alternate names: leukocyte adhesion glycoprotein LFA-1 alpha chain; leukocyte function
C:Species: Homo sapiens (man)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C:Accession: S03308; A47458; A47565; A48759; S36044
R:Larson, R.S.; Corbi, A.L.; Berman, L.; Springer, T.
J. Cell Biol. 108, 703-712, 1989
A:Title: Primary structure of the leukocyte function-associated molecule-1 alpha subunit:
A:Reference number: S03308; MUID:89139587; PMID:2537322
A:Accession: S03308
A:Molecule type: mRNA
A:Residues: 1-1170 <LAR>
A:CROSS-references: UNIPROT:P20701; UNIPROT:09UBC8; EMBL:Y00796; NID:g31421; PIDN:CAA6874
A>Note: part of this sequence was confirmed by protein sequencing
R:Corneill, R.D.; Gollan, K.A.; Hickstein, D.D.
Proc. Natl. Acad. Sci. U.S.A. 90, 4221-4225, 1993
A:Title: Description of the leukocyte function-associated antigen 1 (LFA-1 or CD11a) pr
A:Reference number: A47458; MUID:93248261; PMID:8097887
A:Accession: A47458
A:Molecule type: DNA
A:Residues: 1-20 <COR>
A>Note: sequence extracted from NCBI backbone (NCBIN:130862, NCBI:130863)
R:Shelley, C.S.; Farokhzad, O.C.; Arnaout, M.A.
Proc. Natl. Acad. Sci. U.S.A. 90, 5364-5368, 1993
A:Title: Identification of cell-specific and developmentally regulated nuclear factors t
A:Reference number: A47565; MUID:93281759; PMID:8099450
A:Accession: A47565
A:Molecule type: DNA
A:Residues: 1-20 <SHE>
A:CROSS-references: GB:M95609
R:Nueda, A.; Lopez-Cabrera, M.; Vara, A.; Corbi, A.L.
J. Biol. Chem. 268, 19305-19311, 1993
A:Title: Characterization of the CD11a (alphaL, LFA-1alpha) integrin gene promoter.
A:Reference number: A48759; MUID:93374910; PMID:8103515
A:Accession: A48759
A:Molecule type: DNA
A:Residues: 1-20 <NUE>
A:CROSS-references: EMBL:Z22804; NID:g311405; PIDN:CAA80461.1; PID:g311406
C:Genetics:
A:Gene: GDB:ITGAL; CD11A
A:CROSS-references: GDB:119757; OMIM:153370
A:Map position: 16p11.2-16p11.2
C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homol
C:Keywords: cell adhesion; cytoskeleton; glycoprotein; heterodimer; surface antigen; tra
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-1170/Product: leukocyte adhesion glycoprotein LFA-1 alpha chain #status predicted <
F:154-317/Domain: von Willebrand factor type A repeat homology <VWA2>

Query Match 28.8%; Score 265.5; DB 2; Length 1170;
Best Local Similarity 33.0%; Pred. No. 2.3e-15;
Matches 58; Conservative 44; Mismatches 67; Indels 7; Gaps 2;

QY 1 CPQEDSIAFLIDGSGSIIPHDFFRMKFEVSTVMEQLKKSKTLFSLMOYSEBFRHFTFK 60
DB 150 CIKGNVLDVFLFDGSGSLQDPDEFQKILDFMKDMKLSNNTSYQFAAVQFSTSYKTEFDFS 209
QY 61 EFQNNPRSLVKPTQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 210 DYVKWKDPDALLKHVHMLLLTNTFTGAINYVATEVFEELGAPDPATKLLIITDGE--A 267
QY 121 DPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQCNPE 176
DB 268 TDSGNIDAADK-----IIRYIIGIKHFKQTESQETLHKFASKPASEFVKILDTFE 318

RESULT 6
I56126
lymphocyte fuction-associated molecule-1-alpha - mouse
C:Species: Mus musculus (house mouse)

C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004

C/Accession: I56126
R/Kaufmann, Y.; Tseng, E.; Springer, T.A.
J. Immunol. 147, 369-374, 1991
A>Title: Cloning of the murine lymphocyte function-associated molecule-1 alpha-subunit A
A/Reference number: I56126; MUID:191268576; PMID:2051027
A/Accession: I56126
A/Status: preliminary; translated from GB/EMBL/DBBJ
A/Molecule type: mRNA
A/Residues: 1-1163 <RES>
A/Cross-references: UNIPROT:P24063; GB:M60778; NID:gl98785; PIDN:AAA39426.1; PID:gl98786
C/Genetics:
A/Gene: LFA-1

C/Species: Mus musculus (house mouse)
C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: S66522
R/Aszodi, A.; Hauser, N.; Studer, D.; Paulsson, M.; Hiripi, L.; Bosze, Z.
Eur. J. Biochem. 236, 970-977, 1996
A>Title: Cloning, sequencing and expression analysis of mouse cartilage matrix protein c

A/Reference number: S66522; MUID:96270751; PMID:8665920
A/Accession: S66522
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-500 <ASZ>
A/Cross-references: UNIPROT:P51942; EMBL:U35035; NID:gl163178; PIDN:AA06521.1; PID:gl163

C/Genetics:
A/Gene: CMP
C/Superfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A repeat
F1-29/Domain: signal sequence #status predicted <SIG>
F130-500/Product: cartilage matrix protein #status predicted <MAT>
F43-210/Domain: von Willebrand factor type A repeat homology <VMA1>
F231-266/Domain: EGF homology <EGF>
F:277-441/Domain: von Willebrand factor type A repeat homology <VMA2>

Query Match 26.6%; Score 245; DB 2; Length 1163;
Best Local Similarity 32.6%; Pred. No. 1.5e-13;
Matches 60; Conservative 35; Mismatches 67; Indels 22; Gaps 3;
1 CPQEDSIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEFRHFTFK 60
147 CMKGVDLVFLFDGSGSLDRKDFEKLPEMKDVMKLSNTSYQPAVQFSTDCRTEFTFL 206

61 EF-QNNPRLSVKPIITOLLGTHRTATGIRKVVRELFNITNGARKNAFKILVITDGEK 119
207 DYVKQKNPDVLLGSGVQPMFLITNTFRAINVVAHVFKESGARGPDATKVLVITD 263
120 GDPLGYEDVIPADREG-----VIRYVIGVDAPFRSEKROELNTIASKPRDHVQC 172
264 -----BASDKGNISAAHDITRYIIGKHFVSVQKQKTLHIFASEPVEBFVKIL 312

173 NNFE 176
313 DTFE 316

RESULT 7
A33809
cartilage matrix protein precursor - chicken
C/Species: Gallus gallus (chicken)
C/Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004
C/Accession: A33809; A26364
R/Kiss, I.; Deak, F.; Holloway Jr., R.G.; Delius, H.; Mebust, K.A.; Frimberger, E.; Argu

J. Biol. Chem. 264, 8126-8134, 1989
A>Title: Structure of the gene for cartilage matrix protein, a modular protein of the ex
grins, von Willebrand factor, complement factors B and C2, and epidermal growth factor.
A/Reference number: A33809; MUID:89255246; PMID:2542265
A/Accession: A33809
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-493 <KIS>
A/Cross-references: UNIPROT:P05099; GB:X12346; GB:X12347; GB:X12348; GB:X12349; GB:X1235

R/Argaves, W.S.; Deak, F.; Sparks, K.J.; Kiss, I.; Goetinck, P.F.
Proc. Natl. Acad. Sci. U.S.A. 84, 464-468, 1987
A>Title: Structural features of cartilage matrix protein deduced from cDNA.
A/Reference number: A26364; MUID:87092429; PMID:3025875
A/Accession: A26364
A/Molecule type: mRNA
A/Residues: 78-493 <ARG>
A/Cross-references: GB:M14792; NID:g211545; PIDN:AAA48695.1; PID:g211546

C/Superfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A repe
F37-204/Domain: von Willebrand factor type A repeat homology <VMA1>
F:225-260/Domain: EGF homology <EGF>
F:270-434/Domain: von Willebrand factor type A repeat homology <VMA2>

Query Match 24.6%; Score 227; DB 2; Length 493;
Best Local Similarity 32.0%; Pred. No. 2.1e-12;
Matches 56; Conservative 35; Mismatches 66; Indels 18; Gaps 4;
7 DIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKKS--KTLFSLMOYSEFRHFTFKFQN 64
272 DLVFLIDGSKSVRPENFELVKKFINQIVESLEVSEKQAGLVQYSSVRQEPFLGQFN 331

65 NPNPRLVKPITOLLGTHRTATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLG 124
332 KKDIAKAAVKKAYMEKGTMTQALKYLVDSSFSANGARPGVKGI VFTDGRS----- 385
125 YEDVIPADRE----GVIRYVIGVDAPFRSEKROELNTIASKPRDHVQCNNF 175
386 -QDYITDAAKKAKDLGPRMFAVGNAV-----EDELREIASBPVAHFVYTDADF 434

RESULT 8
S66522
cartilage matrix protein precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: S66522
R/Aszodi, A.; Hauser, N.; Studer, D.; Paulsson, M.; Hiripi, L.; Bosze, Z.
Eur. J. Biochem. 236, 970-977, 1996
A>Title: Cloning, sequencing and expression analysis of mouse cartilage matrix protein c

A/Reference number: S66522; MUID:96270751; PMID:8665920
A/Accession: S66522
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-500 <ASZ>
A/Cross-references: UNIPROT:P51942; EMBL:U35035; NID:gl163178; PIDN:AA06521.1; PID:gl163

C/Genetics:
A/Gene: CMP
C/Superfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A repe
F1-29/Domain: signal sequence #status predicted <SIG>
F130-500/Product: cartilage matrix protein #status predicted <MAT>
F43-210/Domain: von Willebrand factor type A repeat homology <VMA1>
F231-266/Domain: EGF homology <EGF>
F:277-441/Domain: von Willebrand factor type A repeat homology <VMA2>

Query Match 24.1%; Score 222; DB 2; Length 500;
Best Local Similarity 30.5%; Pred. No. 5.9e-12;
Matches 54; Conservative 39; Mismatches 66; Indels 18; Gaps 4;
6 SDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTL--FSLMOYSEFRHFTFKFQ 63
278 TDVFLIDGSKSVRPENFELVKKFINQIVLDVSDRLAQVLVQYSSIRQEPFLGRFH 337
64 NPNPRLSVKPIITOLLGTHRTATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPL 123
338 SKKDIKARVRNVMYKGTMTGAALKYLDLNSFTVSSGARGPQAKVGIVFTDGRS----- 392
124 GYEDVIPADRE----GVIRYVIGVDAPFRSEKROELNTIASKPRDHVQCNNFE 176
393 --QDYINDAARKAKDLGPRMFAVGNAV-----EDELREIASBPVAHFVYTDADF 442

RESULT 9
A37979
cartilage matrix protein precursor - human
C/Species: Homo sapiens (man)
C/Date: 12-Jul-1991 #sequence_revision 12-Jul-1991 #text_change 09-Jul-2004
C/Accession: A37979; B37979
R/Jenkins, R.N.; Osborne-Lawrence, S.L.; Sinclair, A.K.; Eddy Jr., R.L.; Byers, M.G.; Shc
J. Biol. Chem. 265, 19624-19631, 1990
A>Title: Structure and chromosomal location of the human gene encoding cartilage matrix I
A/Reference number: A37979; MUID:91060568; PMID:2246248
A/Accession: A37979
A/Molecule type: DNA
A/Residues: 1-496 <JEN>
A/Cross-references: UNIPROT:P21941; GB:J05667
A/Accession: B37979
A/Molecule type: mRNA
A/Residues: 157-290, 'L', 292-496 <JE2>
A/Cross-references: GB:M55683; GB:J05666; GB:J05667; NID:gl80651; PIDN:AAA63904.1; PID:gl

A: Introns: 32/1; 147/3; 222/1; 264/1; 403/1; 454/1; 481/1
C: Complex: homotrimer
C: Superfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A repeat
C: Keywords: glycoprotein; homotrimer
F: 1-22/Domain: signal sequence #status predicted <SIG>
F: 23-496/Product: cartilage matrix protein #status predicted <MAT>
F: 139-206/Domain: von Willebrand factor type A repeat homology <VWA1>
F: 227-262/Domain: EGF homology <EGF>
F: 273-437/Domain: von Willebrand factor type A repeat homology <VWA2>
F: 76,344/Binding site: carbohydrate (Aan) (covalent) #status predicted
F: 221-236,234-247,249-262/Disulfide bonds: #status predicted

Query Match 23.3%; Score 215; DB 2; Length 496;
Best Local Similarity 29.9%; Pred. No. 2.5e-11;
Matches 53; Conservative 38; Mismatches 68; Indels 18; Gaps 4;

QY 6 SDIAFLDGSGLIIPHDPRRMKEFVSTMEQLKSKTL--PSLMQYSEEFRIHTEFKRFQ 63
DB 274 TDLVFLIDGSKVRPENFELVKKFSQIVDTLDVSDKLAQVGLVQYSSVROEFPFLGRFH 333
QY 64 NNPNRSLVKPTITQLGRTHATGIRKVVRELFNITGARKNAFKILVITDGEKFGDPL 123
DB 334 TKKDIKAARVNSYMEKGTMTGAALKYLIDNSTVSSGARPGAKVGIVFTDGRS---- 388

QY 124 GYEDVIPADRE-----GVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQCNFPE 176
DB 389 --QDYINDAAKAKDLGFMFAGVGNV-----EDELREIASEPVAEHFYFTADFK 438

RESULT 10
S42373
hypothetical protein T20G5.3 - Caenorhabditis elegans
C: Species: Caenorhabditis elegans
C: Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-May-2004
C: Accession: S42373
R: Smith, A.
submitted to the EMBL Data Library, March 1994
A: Reference number: S42368
A: Accession: S42373
A: Molecule type: DNA
A: Residues: 1-3051 <SMT>
A: Cross-references: EMBL:Z30423; NID:G458479; PID:G458485
C: Genes: 96/1; 166/3; 201/2; 355/1; 404/1; 427/2; 794/1; 892/1; 952/2; 1041/1; 1146/1;
F: 512-679/Domain: von Willebrand factor type A repeat homology <VWA1>
F: 754-793/Domain: fibronectin type II repeat homology <2F1>
F: 1201-1244/Domain: EGF homology <EGF>

Query Match 21.3%; Score 196.5; DB 2; Length 3051;
Best Local Similarity 32.2%; Pred. No. 1e-08;
Matches 57; Conservative 36; Mismatches 61; Indels 23; Gaps 7;

QY 1 CPQEDSDIAFLDGSGLIIPHDPRRMKEFVSTMEQLKSKTLPSLMQYSEEFRIH 55
DB 508 CPQKTDVLFLDGSGLSYGVFKNEVRFVFE--LFEIGRSKTRVGLTIQYSDQIRH 565
QY 56 HPTFEFQNNPNRSLVKPITO---LLGRTHATGIRKVVRELFNITGAR---KNAPKI 109
DB 566 EFDLQYGDGD---SLKGISFTQYLTGLTRGAAIQHVQVGFERRGARQQQSDIARV 622

QY 110 LVVITDGEKFGDPLGVEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPR 166
DB 623 AIIITDGRSQDNVTGPAD---SARKLSINTPAIGVTDHVL-----SELESIAGSPNR 672

RESULT 11
A45974
collagen alpha 1(XIV) chain precursor, short form 2 - chicken
N: Alternate names: undulin
C: Species: Gallus gallus (Chicken)
C: Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C: Accession: A45974; S30085; S22916; S17035; S20833
R: Gerecke, D.R.; Foley, J.W.; Castagnola, P.; Gennari, M.; Dublet, B.; Cancedda, R.; Lin

J. Biol. Chem. 268, 12177-12184, 1993
A: Title: Type XIV collagen is encoded by alternative transcripts with distinct 5' regions
A: Reference number: A45974; MUID:93280195; PMID:8505337
A: Accession: A45974
A: Status: preliminary
A: Molecule type: mRNA; protein
A: Residues: 1-1747 <GER>
A: Cross-references: UNIPROT:P32018
A: Experimental source: embryo skin
A: Note: sequence inconsistent with the nucleotide translation
A: Note: sequence extracted from NCBI backbone (NCBIN:133364, NCBIP:133365)
R: Apte, S.S.
submitted to the EMBL Data Library, March 1992
A: Reference number: S30085
A: Accession: S30085
A: Molecule type: mRNA
A: Residues: 1472-1660 <APT>
A: Cross-references: EMBL:X65122; NID:G62871; PIDN:CAA46238.1; PID:G938175
R: Trueb, J.; Trueb, B.
Eur. J. Biochem. 207, 549-557, 1992
A: Title: Type XIV collagen is a variant of undulin.
A: Reference number: S22916; MUID:92339443; PMID:1339349
A: Accession: S22916
A: Status: preliminary
A: Molecule type: mRNA
A: Residues: 286-494, 'Q', 496-834, 'A', 836-1119, 'KL', 1122-1402, 1409-1439 <TRU>
R: Gordon, M.K.; Castagnola, P.; Dublet, B.; Linsenmayer, T.F.; van der Rest, M.; Mayne, F.
Eur. J. Biochem. 201, 333-338, 1991
A: Title: Cloning of a cDNA for a new member of the class of fibril-associated collagens
A: Reference number: S17035; MUID:92037585; PMID:1935930
A: Accession: S17035
A: Molecule type: mRNA
A: Residues: 1472-1659 <GOR1>
A: Accession: S20833
A: Molecule type: protein
A: Residues: 1551-1570; 1593-1599; 1639-1667 <GOR2>
C: Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trimer
F: 40-204/Domain: von Willebrand factor type A repeat homology <VWA1>
F: 236-317/Domain: fibronectin type III repeat homology <FN3A>
F: 326-409/Domain: fibronectin type III repeat homology <FN3B>
F: 418-498/Domain: fibronectin type III repeat homology <FN3C>
F: 507-591/Domain: fibronectin type III repeat homology <FN3D>
F: 625-707/Domain: fibronectin type III repeat homology <FN3E>
F: 716-798/Domain: fibronectin type III repeat homology <FN3F>
F: 806-893/Domain: fibronectin type III repeat homology <FN3G>
F: 924-1089/Domain: von Willebrand factor type A repeat homology <VWA2>
F: 1111-1352/Domain: non-collagenous NC4 #status predicted <NC4>
F: 1511-1552/Domain: non-collagenous NC2 #status predicted <NC2>
F: 1554-1659/Domain: triple helical domain COL1 #status predicted <COL1>

Query Match 21.1%; Score 194.5; DB 2; Length 1747;
Best Local Similarity 31.8%; Pred. No. 7.6e-09;
Matches 57; Conservative 28; Mismatches 83; Indels 11; Gaps 4;

QY 1 CPQEDSDIAFLDGSGLIIPHDPRRMKEFV-STV--MEQLKSKTLPSLMQYSEEFRIH 57
DB 920 CKAARADLVFLVDGSGISGDDNFNFKIISFLYSLGALDKIGPDGTQVAIQFSDDPRTF 979
QY 58 TFKEFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITGARKNAFKILVITDGE 117
DB 980 KLNAYKTETLEAIQQIAYKGGNTKTGAKIHAAREVLFTGBAGMRKGPVKLVWITDGR 1039
QY 118 KFGDPLGVEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQCNFPE 176
DB 1040 SQDD---VNKVSREMLDGFSEFALGVADADYS-----ELVNIGSKPSERHVFVDDDFD 1090

RESULT 12
S31212
collagen alpha 1(XIV) chain precursor, short form - chicken
C: Species: Gallus gallus (Chicken)
C: Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 15-Sep-2003

C:Accession: S31212
R:Waelchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B.
Eur. J. Biochem. 212, 483-490, 1993
A:Title: Complete primary structure of chicken collagen XIV.
A:Reference number: S31211; MUID:93185668; PMID:8444186
A:Accession: S31212
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-1857 <WAE>
A:Cross-references: EMBL:X70792; NID:g288874; PIDN:CAA50063.1; PID:g288875
A:Note: The nucleotide sequence was submitted to the EMBL Data Library, January 1993
C:Genetics:
A:Gene: Coll14A1
C:Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trimer
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-1857/Product: collagen alpha 1(XIV) chain, short form #status predicted <WAT>
F:29-110/Domain: fibronectin type III repeat homology <FN3A>
F:156-320/Domain: von Willebrand factor type A repeat homology <VWAL>
F:352-433/Domain: fibronectin type III repeat homology <FN3B>
F:442-525/Domain: fibronectin type III repeat homology <FN3C>
F:534-614/Domain: fibronectin type III repeat homology <FN3D>
F:623-707/Domain: fibronectin type III repeat homology <FN3E>
F:741-823/Domain: fibronectin type III repeat homology <FN3F>
F:832-914/Domain: fibronectin type III repeat homology <FN3G>
F:922-1009/Domain: fibronectin type III repeat homology <FN3H>
F:1040-1205/Domain: von Willebrand factor type A repeat homology <VWAL2>
Query Match 21.1%; Score 194.5; DB 2; Length 1857;
Best Local Similarity 31.8%; Pred. No. 8.2e-09;
Matches 57; Conservative 28; Mismatches 83; Indels 11; Gaps 4;
C:Species: Gallus gallus (chicken)
C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
C:Accession: S78476; S31211
R:Trueb, B.
submitted to the EMBL Data Library, January 1993
A:Reference number: S78476
A:Accession: S78476
A:Molecule type: mRNA
A:Residues: 1-1888 <TRU>
A:Cross-references: UNIPROT:P32018; EMBL:X70793; NID:g288872; PIDN:CAA50064.1; PID:g288874
R:Waelchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B.
Eur. J. Biochem. 212, 483-490, 1993
A:Title: Complete primary structure of chicken collagen XIV.
A:Reference number: S31211; MUID:93185668; PMID:8444186
A:Accession: S31211
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-416,1460-1811,1843-1888 <WAE>
A:Cross-references: EMBL:X70793
C:Genetics:
A:Gene: Coll14A1
C:Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trimer
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-1888/Product: collagen alpha 1(XIV) chain, long form #status predicted <WAT>
F:29-110/Domain: fibronectin type III repeat homology <FN3A>
F:156-320/Domain: von Willebrand factor type A repeat homology <VWAL>

F:352-433/Domain: fibronectin type III repeat homology <FN3B>
F:442-525/Domain: fibronectin type III repeat homology <FN3C>
F:534-614/Domain: fibronectin type III repeat homology <FN3D>
F:623-707/Domain: fibronectin type III repeat homology <FN3E>
F:741-823/Domain: fibronectin type III repeat homology <FN3F>
F:832-914/Domain: fibronectin type III repeat homology <FN3G>
F:922-1009/Domain: fibronectin type III repeat homology <FN3H>
F:1040-1205/Domain: von Willebrand factor type A repeat homology <VWAL2>
Query Match 21.1%; Score 194.5; DB 2; Length 1888;
Best Local Similarity 31.8%; Pred. No. 8.4e-09;
Matches 57; Conservative 28; Mismatches 83; Indels 11; Gaps 4;
C:Species: Gallus gallus (chicken)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A40020; A34485; A28037; S23814; S22254; S28811
R:Yamagata, M.; Yamada, K.M.; Yamada, S.S.; Shinomura, T.; Tanaka, H.; Nishida, Y.; Obara, J. Cell Biol. 115, 209-221, 1991
A:Title: The complete primary structure of type XII collagen shows a chimeric molecule with a region of type IX collagen, and short collagenous domains with an Arg-Gly-Asp site.
A:Reference number: A40020; MUID:92011862; PMID:1918137
A:Accession: A40020
A:Molecule type: mRNA
A:Residues: 1-3124 <YAM>
A:Cross-references: UNIPROT:P13944; GB:D00824; NID:g222810; PIDN:BA00701.1; PID:g222811
A:Note: in the authors' translation residues 1216-1219 are shown after residue 1235 and, R:Gordon, M.K.; Gerecke, D.R.; Dublet, B.; van der Rest, M.; Olsen, B.R.
J. Biol. Chem. 264, 19772-19778, 1989
A:Title: Type XII collagen. A large multidomain molecule with partial homology to type I
A:Reference number: A34485; MUID:90062079; PMID:2584192
A:Accession: A34485
A:Molecule type: mRNA
A:Residues: 2456-2758, 'A', 2760-2802, 'F', 2804-2976, 'F', 2978-3124 <GOR>
A:Cross-references: EMBL:J05137; NID:g211284; PIDN:AAA48635.1; PID:g211285
A:Accession: B34485
A:Molecule type: protein
A:Residues: 2772-2792; 2846-2873 <GOR2>
R:Gordon, M.K.; Gerecke, D.R.; Olsen, B.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 6040-6044, 1987
A:Title: Type XII collagen: distinct extracellular matrix component discovered by cDNA c
A:Reference number: A28037; MUID:87317590; PMID:3476925
A:Accession: A28037
A:Molecule type: mRNA
A:Residues: 2960-2976, 'F', 2978-3074, 'AG', <GOR3>
A:Cross-references: EMBL:M17375; NID:g211649; PIDN:AAA48718.1; PID:g211650
A:Note: this sequence has been revised in reference A34485
R:Koch, M.; Bernasconi, C.; Chiquet, M.
Eur. J. Biochem. 207, 847-856, 1992
A:Title: A major oligomeric fibroblast proteoglycan identified as a novel large form of t
A:Reference number: S23814; MUID:92362621; PMID:1323460
A:Accession: S23814
A:Molecule type: protein
A:Residues: 'X', 1333, 'Q', 1335-1347; 1914-1928; 2504, 'X', 2506, 'X', 2508-2511, 'X', 2513-2517 <
R:Dublet, B.; van der Rest, M.
J. Biol. Chem. 262, 17724-17727, 1987
A:Title: Type XII collagen is expressed in embryonic chick tendons. Isolation of pepsin-

A:Reference number: S22254; MUID:89087065; PMID:3121603
A:Accession: S22254
A:Molecule type: protein
A:Residues: 2831-2832,'T',2834,'R',2836-2843;3002-3014 <DUB>
R:Trueb, J.; Trueb, B.
Biochim. Biophys. Acta 1171, 97-98, 1992
A:Title: The two splice variants of collagen XII share a 'common 5' end.
A:Reference number: S28811; MUID:93042014; PMID:1420368
A:Accession: S28811
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-24,1189-1257,'S',1259-1263,'E',1265-1280 <TRU>
A:Cross-references: EMBL:X67327

C:Genetics:
A:Introns: 2845/3; 2863/3; 2887/3; 2899/3; 2922/1; 2985/1; 3008/1; 3065/1
C:Keywords: alternative splicing; cell binding; coiled coil; connective tissue; disulfide
C:1-23/Domain: signal sequence #status predicted <SIG>
F:24-3124/Product: collagen alpha 1(XII) chain #status predicted <MAT>
F:24,1189-3124/Product: collagen alpha 1(XII) chain short splice form #status predicted
F:24,1184/Domain: IIIA #status predicted <IIIA>
F:24-105/Domain: fibronectin type III repeat homology <VWAL>
F:137-301/Domain: von Willebrand factor type A repeat homology <VWAL>
F:332-425/Domain: IIIB #status predicted <IIIB>
F:332-414/Domain: fibronectin type III repeat homology <FN3B>
F:433-601/Domain: von Willebrand factor type A repeat homology <VWA2>
F:629-1178/Domain: IIIC #status predicted <IIIC>
F:630-711/Domain: fibronectin type III repeat homology <FN3C>
F:721-802/Domain: fibronectin type III repeat homology <FN3D>
F:812-895/Domain: fibronectin type III repeat homology <FN3E>
F:905-986/Domain: fibronectin type III repeat homology <FN3F>
F:993-1076/Domain: fibronectin type III repeat homology <FN3G>
F:1086-1169/Domain: fibronectin type III repeat homology <FN3H>
F:1197-1361/Domain: von Willebrand factor type A repeat homology <VWA3>
F:1384-2295/Domain: IIID #status predicted <IIID>
F:1384-1465/Domain: fibronectin type III repeat homology <FN3I>
F:1474-1557/Domain: fibronectin type III repeat homology <FN3J>
F:1566-1647/Domain: fibronectin type III repeat homology <FN3K>
F:1655-1738/Domain: fibronectin type III repeat homology <FN3L>
F:1756-1838/Domain: fibronectin type III repeat homology <FN3M>
F:1847-1928/Domain: fibronectin type III repeat homology <FN3N>
F:1937-2019/Domain: fibronectin type III repeat homology <FN3O>
F:2028-2110/Domain: fibronectin type III repeat homology <FN3P>
F:2119-2199/Domain: fibronectin type III repeat homology <FN3Q>
F:2207-2294/Domain: fibronectin type III repeat homology <FN3R>
F:2325-2490/Domain: von Willebrand factor type A repeat homology <VWA4>
F:2438-2440/Region: cell adhesion #status predicted
F:2509-2750/Domain: IXP, homologous to NC4 domain of type IX collagen #status predicted
F:2751-2902/Domain: collagen COL2 #status predicted <COL2>
F:2899-2901/Region: cell attachment (R-G-D) motif
F:2903-2945/Domain: non-collagenous NC2 #status predicted <NC2>
F:2946-3048/Domain: collagenous COL1 #status predicted <COL1>
F:3049-3124/Domain: non-collagenous NC1 #status predicted <NC1>
F:32,1006,1032,1044,1512,1767,2210,2273,2532,2683/Binding site: carbohydrate (Asn) (cova
F:2780,2789,2836,2842,2860,2866,2869,3004,3007/Modified site: hydroxyproline (Pro) #stat

Query Match 20.8%; Score 192; DB 2; Length 3124;
Best Local Similarity 29.9%; Pred. No. 2.6e-08;
Matches 53; Conservative 34; Mismatches 72; Indels 18; Gaps 4;
QY 6 SDIAPLDGSGSIIPHDPRRMKEFVSTVME--QLKSKTLFLSMQYSEEFRIHFTKFEQ 63
DB 138 TDVLFLVDGWSVGRNFRYILDVAFDVGEEKTRGVGVQVSSDTRTFEFLNQYF 197
QY 64 NNPNRSLVKPITQLLGRTHATGIRKVVRELFNTNGARKNAFKILVVTIDGKFGDPL 123
DB 198 RRSDDLDAIKRIPYKGGTWTGEADYLVKNTFTSAGARKGPKPAIVITDGA----- 252

QY 124 GYEDVIPEADREGVIRYVIGVDAPR-----SEKSRQELNTIASKPPRDHVFQCN 176
DB 253 --QDEVEIPARELNRIGVEVSLGIAK-----DAKELKLIASQPSLKHVFNVANFD 302

RESULT 15

A45226
Integrin alpha-1 chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A45226
R:Briesewitz, R.; Epstein, M.R.; Marcantonio, E.E.
J. Biol. Chem. 268, 2989-2996, 1993
A:Title: Expression of native and truncated forms of the human integrin alpha 1 subunit.
A:Reference number: A45226; MUID:93155124; PMID:8428973
A:Accession: A45226
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1151 <BRI>
A:Cross-references: UNIPROT:P56199
A:Experimental source: hepatoblastoma cell line HepG2
A:Note: sequence extracted from NCBI backbone (NCBIP:124326)
F:142-317/Domain: von Willebrand factor type A repeat homology <VWAL>

Query Match 20.2%; Score 186.5; DB 2; Length 1151;
Best Local Similarity 28.4%; Pred. No. 2.3e-08;
Matches 50; Conservative 37; Mismatches 78; Indels 11; Gaps 5;
QY 7 DIAPLDGSGSIIPHDPRRMKEFVSTVMEQLK--KSKTLFLSMQYSEEFRIHFTKFEQ 64
DB 144 DIVIVLDGSGSIIPWD--SVTAFNLDLKRMIDIGPKQTVGVQVGVNTHFNLNKYS 201
QY 65 NNPNRSLVKPITQLLGRTHATGIRKVVRELFNTNGARKNAFKILVVTIDGKFGDPL 123
DB 202 TEEVLVAAKIVQRGGRQTMTALGTDARKEAFTEARGARRGVKKVMVITVDGESH-DNH 260
QY 124 GYEDVIPEADREGVIRYVIGVDAPR-----SEKSRQELNTIASKPPRDHVFQCN 174
DB 261 RLKKVIQDCEDENIQRFSAIILGNSYRGNLSTEKEFVERIKSIASBPTKEKHFNVSD 316

Search completed: January 13, 2005, 15:13:31
Job time : 6.12706 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2005, 15:04:07 ; Search time 37.0546 Seconds
(without alignments)
2748.409 Million cell updates/sec

Title: RWHULB-C_COPY_144_320
Perfect score: 922
Sequence: 1 CPQEDSDIAFLIDSGSIIP.....NTIASKPPRDHVFQCNPEC.177

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt.02.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	903	97.9	1152	1	ITAM_HUMAN	P11215 homo sapien
2	722	78.3	920	2	Q28984	Q28984 sus scrofa
3	692	75.1	1153	1	ITAM_MOUSE	P05555 mus musculus
4	669	72.6	1151	2	Q9J130	Q9J130 rattus norv
5	550	59.7	1161	1	ITAD_RAT	Q9QY67 rattus norv
6	545	59.1	1162	1	ITAD_HUMAN	P13349 homo sapien
7	533	57.8	205	2	Q63001	Q63001 rattus norv
8	486	52.7	1163	1	ITAX_HUMAN	P20702 homo sapien
9	483	52.4	1188	2	Q6KAS4	Q6KAS4 mus musculus
10	483	52.4	1188	2	BAD21383	Bad21383 mus muscu
11	482	52.3	1169	1	ITAX_MOUSE	Q9QX44 mus musculus
12	408	44.3	304	2	Q6PG66	Q6PG66 mus musculus
13	408	44.3	304	2	AAH57200	AAH57200 mus muscu
14	322	34.9	895	2	Q9WUF8	Q9WUF8 mus sp. itg
15	322	34.9	1038	2	Q8BS01	Q8BS01 mus musculus
16	322	34.9	1167	2	Q88340	Q88340 rattus norv
17	319	34.6	231	2	Q8N882	Q8N882 homo sapien
18	316	34.3	1167	1	ITAE_MOUSE	Q60677 mus musculus
19	309	33.5	1179	1	ITAE_HUMAN	P38570 homo sapien
20	307	33.3	1160	2	Q8MKF4	Q8MKF4 felis silve
21	301.5	32.7	1167	2	Q88341	Q88341 rattus norv
22	269.5	29.2	1170	1	ITAL_HUMAN	P20701 homo sapien
23	262.5	28.5	1165	1	ITAL_BOVIN	P61625 bos taurus
24	256	27.8	269	2	Q80WE9	Q80WE9 rattus norv
25	245	26.6	1160	2	Q9R200	Q9R200 mus musculus
26	245	26.6	1161	2	Q9WTV4	Q9WTV4 mus musculus
27	245	26.6	1163	1	ITAL_MOUSE	P24063 mus musculus
28	240.5	26.1	1196	2	Q98TF1	Q98TF1 cyprinus ca
29	238.5	25.9	1166	2	Q6TYB8	Q6TYB8 bos taurus
30	238.5	25.9	1166	2	AAQ90015	AAQ90015 bos tauru
31	238	25.8	257	2	Q8C270	Q8C270 mus musculus

32	235	25.5	79	2	Q8HY27	Q8HY27 ovis aries
33	235	25.5	79	2	Q8HY41	Q8HY41 bos taurus
34	227	24.6	493	1	CAMA_CHICK	P05099 gallus gall
35	226.5	24.6	1187	2	Q98TFO	Q98TFO cyprinus ca
36	222.5	24.1	652	2	Q95LI2	Q95LI2 bos taurus
37	222	24.1	500	1	CAMA_MOUSE	P51942 mus musculus
38	222	24.1	500	2	Q8OVN5	Q8OVN5 mus musculus
39	220.5	23.9	656	2	Q96DT1	Q96DT1 homo sapien
40	220.5	23.9	678	2	Q9UDN0	Q9UDN0 homo sapien
41	220.5	23.9	678	2	AAQ88704	AAQ88704 homo sapi
42	220.5	23.9	693	2	Q96DM8	Q96DM8 homo sapien
43	215	23.3	496	1	CAMA_HUMAN	P21941 homo sapien
44	210.5	22.8	650	2	Q8VHI5	Q8VHI5 mus musculus
45	208.5	22.6	628	2	Q8BQ41	Q8BQ41 mus musculus

ALIGNMENTS

RESULT 1
ITAM_HUMAN
ID ITAM_HUMAN STANDARD; PRT; 1152 AA.
AC P11215;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha subunit) (CR-3 alpha chain) (CD11b) (leukocyte adhesion receptor MOI)
DE (Neutrophil adherence receptor).
GN Name=ITGAM; Synonyms=CR3A, CD11b;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88315033; PubMed=2457584;
RA Corbi A.L., Kishimoto T.K., Miller L.J., Springer T.A.;
RT "The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, CD11b) alpha subunit. Cloning, primary structure, and relation to the integrins, von Willebrand factor and factor B.";
RL J. Biol. Chem. 263:12403-12411(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88190151; PubMed=2833753;
RA Arnaout M.A., Remold-O'Donnell E., Pierce M.W., Harris P., Tenen D.G.;
RT "Molecular cloning of the alpha subunit of human and guinea pig leukocyte adhesion glycoprotein Mol: chromosomal localization and homology to the alpha subunits of integrins.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:2776-2780(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88257215; PubMed=2454931;
RA Arnaout M.A., Gupta S.K., Pierce M.W., Tenen D.G.;
RT "Amino acid sequence of the alpha subunit of human leukocyte adhesion receptor Mol (complement receptor type 3).";
RL J. Cell Biol. 106:2153-2158(1988).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=93123748; PubMed=8419480;
RA Fleming J.C., Pahl H.L., Gonzalez D.A., Smith T.F., Tenen D.G.;
RT "Structural analysis of the CD11b gene and phylogenetic analysis of the alpha-integrin gene family demonstrate remarkable conservation of genomic organization and suggest early diversification during evolution.";
RL J. Immunol. 150:480-490(1993).
RN [5]
RP SEQUENCE OF 9-1153 FROM N.A.
RX MEDLINE=8909893; PubMed=2563162;
RA Hackett D.D., Hickey M.J., Ozols J., Baker D.M., Back A.L., Roth G.J.;
RT "cDNA sequence for the alpha M subunit of the human neutrophil adherence receptor indicates homology to integrin alpha subunits.";

Proc. Natl. Acad. Sci. U.S.A. 86:257-261 (1989).
[6] SEQUENCE OF 1-9 FROM N.A.
RX MEDLINE=92073318; PubMed=1683702;
RA Shelley C.S., Arnaut M.A.;
RT "The promoter of the CD11b gene directs myeloid-specific and
developmentally regulated expression.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:10525-10529 (1991).
[7] SEQUENCE OF 1-9 FROM N.A.
RX MEDLINE=87076671; PubMed=3539202;
RA Pierce M.W., Remold-O'Donnell E., Todd R.F. III, Arnaut M.A.;
RT "N-terminal sequence of human leukocyte glycoprotein Mol: conservation
across species and homology to platelet IIb/IIIa.";
RL Biochim. Biophys. Acta 874:368-371 (1986).
[9] X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 148-331.
RX MEDLINE=95171458; PubMed=7867070;
RA Lee J.O., Kieu P., Arnaut M.A., Liddington R.;
RT "Crystal structure of the A domain from the alpha subunit of integrin
CR3 (CD11b/CD18).";
RL Cell 80:631-638 (1995).
[10] X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 148-334.
RX MEDLINE=96363671; PubMed=8747460;
RA Lee J.O., Bankston L.A., Arnaut M.A., Liddington R.C.;
RT "Two conformations of the integrin A-domain (I-domain): a pathway for
activation?";
RL Structure 3:1333-1340 (1995).
[11] X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 148-337.
RX MEDLINE=98362595; PubMed=9687375;
RA Baldwin E.T., Sarver R.W., Bryant G.L. Jr., Curry K.A.,
FAirbanks M.B., Finzel B.C., Garlick R.L., Heinrikson R.L.,
Horton N.C., Kelley L.L., Milder A.M., Moon J.B., Mott J.E.,
Mutchler V.T., Tomich C.S., Watenpaugh K.D., Wiley V.H.;
RT "Cation binding to the integrin CD11b I domain and activation model
assessment.";
RL Structure 6:923-935 (1998).
[12] 3D-STRUCTURE MODELING OF 17-616.
RX MEDLINE=98226734; PubMed=9560195;
RA Oxvig C., Springer T.A.;
RT "Experimental support for a beta-propeller domain in integrin alpha-
subunits and a calcium binding site on its lower surface.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:4870-4875 (1998).
CC -1- FUNCTION: Integrin alpha-M/beta-2 is implicated in various
adhesive interactions of monocytes, macrophages and granulocytes
as well as in mediating the uptake of complement-coated particles.
It is identical with CR-3, the receptor for the iC3b fragment of
the third complement component. It probably recognizes the R-G-D
peptide in C3b. Integrin alpha-M/beta-2 is also a receptor for
fibrinogen, factor X and ICAM1. It recognizes P1 and P2 peptides
of fibrinogen gamma chain.
CC -1- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-M
associates with beta-2.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Predominantly expressed in monocytes and
granulocytes.
CC -1- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins
with I-domains do not undergo protease cleavage.
CC -1- SIMILARITY: Belongs to the integrin alpha chain family.
CC -1- SIMILARITY: Contains 7 FG-GAP repeats.
CC -1- SIMILARITY: Contains 1 VWFA domain.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD11b entry;
WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd11b.htm".

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or send an email to license@isb-sib.ch).

EMBL; J03925; AAA59544.1; -
EMBL; M18044; AAA59491.1; -
EMBL; J04145; AAA59903.1; -
EMBL; S52227; AAB24821.1; -
EMBL; S52152; AAB24821.1; JOINED.
EMBL; S52153; AAB24821.1; JOINED.
EMBL; S52154; AAB24821.1; JOINED.
EMBL; S52155; AAB24821.1; JOINED.
EMBL; S52157; AAB24821.1; JOINED.
EMBL; S52159; AAB24821.1; JOINED.
EMBL; S52161; AAB24821.1; JOINED.
EMBL; S52164; AAB24821.1; JOINED.
EMBL; S52165; AAB24821.1; JOINED.
EMBL; S52167; AAB24821.1; JOINED.
EMBL; S52169; AAB24821.1; JOINED.
EMBL; S52170; AAB24821.1; JOINED.
EMBL; S52173; AAB24821.1; JOINED.
EMBL; S52174; AAB24821.1; JOINED.
EMBL; S52180; AAB24821.1; JOINED.
EMBL; S52181; AAB24821.1; JOINED.
EMBL; S52184; AAB24821.1; JOINED.
EMBL; S52189; AAB24821.1; JOINED.
EMBL; S52191; AAB24821.1; JOINED.
EMBL; S52192; AAB24821.1; JOINED.
EMBL; S52203; AAB24821.1; JOINED.
EMBL; S52212; AAB24821.1; JOINED.
EMBL; S52213; AAB24821.1; JOINED.
EMBL; S52216; AAB24821.1; JOINED.
EMBL; S52219; AAB24821.1; JOINED.
EMBL; S52220; AAB24821.1; JOINED.
EMBL; S52221; AAB24821.1; JOINED.
EMBL; S52222; AAB24821.1; JOINED.
EMBL; S52226; AAB24821.1; JOINED.
EMBL; M76724; AAA58410.1; -
EMBL; M84477; AAA51960.1; -
PIR; A31108; RWHU1B.
PDB; 1A8X; Model; @=17-1152.
PDB; 1BHO; X-ray; 1/2=-.
PDB; 1BHQ; X-ray; 1/2=-.
PDB; 1IDN; X-ray; 1/2=-.
PDB; 1IDO; X-ray; @=140-331.
PDB; 1JLM; X-ray; @=143-334.
PDB; 1MU; X-ray; A=137-331.
PDB; 1NF7; X-ray; A=144-337.
PDB; 1N9Z; X-ray; A=140-335.
PDB; 1NAS; X-ray; A=144-345.
Genew; HGNC:6149; ITGAM.
MIM; 120980; -
GO; GO:0008305; C:integrin complex; TAS.
GO; GO:0007155; P:cell adhesion; TAS.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; VWFA.
Pfam; PF01839; FG-GAP; 3.
Pfam; PF00357; Integrin_alpha; 1.
Pfam; PF00092; VWFA; 1.
PRINTS; PR01185; INTEGRINA.
PRINTS; PR00453; VWFADOMAIN.
SMART; SM00191; Int_alpha; 5.
SMART; SM00327; VWFA; 1.
PROSITE; PS00242; INTEGRIN_ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
3D-structure; Calcium; Cell adhesion; Direct protein sequencing;
KW Glycoprotein; Integrin; Magnesium; Receptor; Repeat; Signal;
KW Transmembrane.

```
FT SIGNAL 1 16 Integrin alpha-M.
FT CHAIN 17 1152

Query Match
Best Local Similarity 97.9%; Score 903; DB 1; Length 1152;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CPQSDIAFLIDGSGSIIPHDPRMKGFSVTVMSQLKKSKTLFSLMQYSEFRHFTFK 60
Db 144 CPQSDIAFLIDGSGSIIPHDPRMKGFSVTVMSQLKKSKTLFSLMQYSEFRHFTFK 203

Qy 61 EFQNNPNRSLVKPITOLLGRTHHTATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
Db 204 EFQNNPNRSLVKPITOLLGRTHHTATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 263

Qy 121 DPLGYEDVPEADREGVIRYVIGVDGAFRSEKSRQELNTIASKPPRDHVFQCNFFE 176
Db 264 DPLGYEDVPEADREGVIRYVIGVDGAFRSEKSRQELNTIASKPPRDHVFQCNFFE 319

RESULT 2
Q28984 PRELIMINARY; PRT; 920 AA.
AC Q28984;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE CD11b (Fragment).
GN Name=CD11b;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee J.-K., Schook L.B., Rutherford M.S.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBSJ databases.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
DR EMBL; U40072; AAB16869.1; -
DR GO; GO:0008305; C:integrin complex; IEA.
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR InterPro; IPR000413; Integrin_alpha.
DR Pfam; PF01839; FG-GAP; 3.
DR Pfam; PF00092; VWA; 1.
DR PRINTS; PR01185; INTEGRINA.
DR SMART; SM00191; Int_alpha; 4.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS50234; VWPA; 1.
KW Cell adhesion; Integrin; Transmembrane.
FT NON_TER 1
FT NON_TER 920
SQ SEQUENCE 920 AA; 102440 MW; E96CC51E350DD5AC CRC64;

Query Match
Best Local Similarity 80.1%; Score 722; DB 2; Length 920;
Matches 141; Conservative 16; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CPQSDIAFLIDGSGSIIPHDPRMKGFSVTVMSQLKKSKTLFSLMQYSEFRHFTFK 60
Db 11 CPQSDIAFLIDGSGSIINRLDFQRMKGFSVTVMSQGFQKSKTLFALMQYSEDFYTHFTFN 70

Qy 61 EFQNNPNRSLVKPITOLLGRTHHTATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
Db 71 DFKRPNPSKLLVRPRLQLGRTHHTATGIRKVVRELFHSGSGARENALKILVITDGEKFG 130

Qy 121 DPLGYEDVPEADREGVIRYVIGVDGAFRSEKSRQELNTIASKPPRDHVFQCNFFE 176
Db 131 DPLGYEDVPEADRGKGVIRYVIGVDGAFNSWRSRELNTIASKPCGDHVFQCNFFE 186
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RESULT 3
ITAM_MOUSE
ID ITAM_MOUSE STANDARD; PRT; 1153 AA.
AC P05555; O8CAV73;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DE Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor MO1).
DE subunit (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor MO1).
GN Name=Itgam;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=88312584; PubMed=3044779;
RA Pytela R.;
RT "Amino acid sequence of the murine Mac-1 alpha chain reveals homology with the integrin family and an additional domain related to von Willebrand factor."
RL EMBO J. 7:1371-1378(1988).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Niikaido I., Osato N., Saito R., Suzuki H., Yamanaoka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Baldarilli R., Hill D.P., Sult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lennhard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Sempie C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verdaro R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wyszynski-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Alizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RN [3]
RP SEQUENCE OF 11-45 FROM N.A.
RC STRAIN=BALB/c; TISSUE=Spleen;
RX MEDLINE=86287312; PubMed=2942940;
RA Sastre L., Roman J.M., Teplow D.B., Dreyer W.J., Gee C.E., Larson R.S., Roberts T.M., Springer T.A.;
RT "A partial genomic DNA clone for the alpha subunit of the mouse complement receptor type 3 and cellular adhesion molecule Mac-1."
RL Proc. Natl. Acad. Sci. U.S.A. 83:5644-5648(1986).
RN [4]
RP SEQUENCE OF 17-28.
RX MEDLINE=85188276; PubMed=3887182;
RA Springer T.A., Teplow D.B., Dreyer W.J.;
RT "Sequence homology of the LFA-1 and Mac-1 leukocyte adhesion glycoproteins and unexpected relation to leukocyte interferon."
RL Nature 314:540-542(1985).
CC -!- FUNCTION: Integrin alpha-M/beta-2 is implicated in various adhesive interactions of monocytes, macrophages and granulocytes
```

as well as in mediating the uptake of complement-coated particles. It is identical with CR-3, the receptor for the iC3b fragment of the third complement component. It probably recognizes the R-G-D peptide in C3b. Integrin alpha-M/beta-2 is also a receptor for fibrinogen, factor X and ICAM1. It recognizes P1 and P2 peptides of fibrinogen gamma chain. Alpha-M/beta-2 play a critical role in mast cell development and in immune complex-mediated glomerulonephritis. Mice expressing a null mutation of the alpha-M subunit gene demonstrate increase in neutrophil accumulation, in response to a impaired degradation and phagocytosis, events that apparently accelerate apoptosis in neutrophils. These mice develop obesity.

-!- SUBUNIT: Heterodimer of an alpha and a beta chain. Alpha-M associates with beta-2.

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;

Name=1;

Isoid=P05555-1; Sequence=Displayed;

Name=2;

Isoid=P05555-2; Sequences=VSP_010473;

Notes=No experimental confirmation available;

TISSUE SPECIFICITY: Predominantly expressed in monocytes and granulocytes.

-!- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.

-!- SIMILARITY: Belongs to the integrin alpha chain family.

-!- SIMILARITY: Contains 7 FG-GAP repeats.

-!- SIMILARITY: Contains 1 VWFA domain.

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EMBL; X07640; CAA30479.1; -.

EMBL; AK039444; BAC30350.1; -.

EMBL; M14293; AAA39484.1; -.

PIR; S00551; S00551.

HSP; P11215; 1BHQ.

MGI; 96607; Itgam.

GO; GO:0009897; C:external side of plasma membrane; IDA.

GO; GO:0007155; P:cell adhesion; IMP.

GO; GO:0045123; P:cellular extravasation; IMP.

GO; GO:0030593; P:neutrophil chemotaxis; IMP.

InterPro; IPR000413; Integrin_alpha.

InterPro; IPR002035; VWF A.

Pfam; PF01839; FG-GAP; 3.

Pfam; PF00357; Integrin_alpha; 1.

Pfam; PF00092; VWF; 1.

PRINTS; PR01185; INTEGRINA.

PRINTS; PR00453; VWFADOMAIN.

SMART; SM00191; Int_alpha; 5.

SMART; SM00327; VWF; 1.

PROSITE; PS00242; INTEGRIN_ALPHA; 1.

PROSITE; PS0234; VWFA; 1.

Alternative splicing; Calcium; Cell adhesion; Integrin; Receptor; Repeat; Direct protein sequencing; Glycoprotein; Integrin; Receptor; Repeat; Signal; Transmembrane.

SIGNAL 1 16

CHAIN 17 1153 Integrin alpha-M.

DOMAIN 17 1105 Extracellular (Potential).

TRANSMEM 1106 1129 Potential.

DOMAIN 1130 1153 Cytoplasmic (Potential).

REPEAT 31 84 FG-GAP 1.

REPEAT 85 163 FG-GAP 2.

DOMAIN 164 350 VWFA.

REPEAT 337 400 FG-GAP 3.

REPEAT 401 452 FG-GAP 4.

REPEAT 454 515 FG-GAP 5.

REPEAT 517 575 FG-GAP 6.

REPEAT 580 632 FG-GAP 7.

CA_BIND 465 473 Potential.

CA_BIND 529 537 Potential.

CA_BIND 592 600 Potential.

SITE 1132 1136 GFFKR motif.

DISULFID 66 73 By similarity.

DISULFID 105 123 By similarity.

DISULFID 654 711 By similarity.

DISULFID 770 776 By similarity.

DISULFID 999 1023 By similarity.

DISULFID 1028 1033 By similarity.

CARBOHYD 58 58 N-linked (GlcNAc...) (Potential).

CARBOHYD 86 86 N-linked (GlcNAc...) (Potential).

CARBOHYD 391 391 N-linked (GlcNAc...) (Potential).

CARBOHYD 696 696 N-linked (GlcNAc...) (Potential).

CARBOHYD 734 734 N-linked (GlcNAc...) (Potential).

CARBOHYD 772 772 N-linked (GlcNAc...) (Potential).

CARBOHYD 801 801 N-linked (GlcNAc...) (Potential).

CARBOHYD 881 881 N-linked (GlcNAc...) (Potential).

CARBOHYD 907 907 N-linked (GlcNAc...) (Potential).

CARBOHYD 941 941 N-linked (GlcNAc...) (Potential).

CARBOHYD 980 980 N-linked (GlcNAc...) (Potential).

CARBOHYD 994 994 N-linked (GlcNAc...) (Potential).

CARBOHYD 1022 1022 N-linked (GlcNAc...) (Potential).

CARBOHYD 1045 1045 N-linked (GlcNAc...) (Potential).

CARBOHYD 1051 1051 N-linked (GlcNAc...) (Potential).

CARBOHYD 1076 1076 N-linked (GlcNAc...) (Potential).

VARSPLIC 453 569 Missing (in isoform 2).

CONFLICT 37 37 N -> S (in Ref. 2).

CONFLICT 683 683 V -> G (in Ref. 2).

SEQUENCE 1153 AA; 127480 MW; 178DB988AECB0343 CRC64;

Query Match 75.1%; Score 692; DB 1; Length 1153;

Best Local Similarity 77.3%; Pred. No. 3.6e-49;

Matches 136; Conservative 18; Mismatches 22; Indels 0; Gaps 0;

QY 1 CPQSDSIAFLIDGSGSIIPHDFFRMKEFVSTVMQELKKSKTLFSLMQYSEPRHFTFK 60

DB 144 CPQESDIVFLIDGSGSINNIDFQKKEFVSTVMQELKKSKTLFSLMQYSEPRHFTFN 203

QY 61 BFQNNPRLVKDITQLLGHGTHATGIRKVVRLFNITGARKNAKILVITDGEKFG 120

DB 204 DFKRNPSPRSHVSPIKQLNGTKTASGIRKVVRLFNITGARKNAKILVITDGEKFG 263

QY 121 DPLGYEDVPEADREGVIRVVGVDAPFRSEKSKQLNTIASKPPRDHVFQNNFE 176

DB 264 DPLDYKDVPEADRAGVIRVVGVDAPFRSEKSKQLNTIASKPPRDHVFQNNFE 319

RESULT 4

Q9J130 PRELIMINARY; PRT; 1151 AA.

ID Q9J130 PRELIMINARY;

AC Q9J130; TREMBLrel. 15, Created

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-OCT-2000 (TREMBLrel. 26, Last annotation update)

DE Integrin beta 2 alpha subunit.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI_TaxID=10116;

SEQUENCE FROM N.A.

RA Fathallah D.M. Sr., Zeria K. Jr.;

RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

CC -!- SIMILARITY: Belongs to the integrin alpha chain family.

DR EMBL; AF268593; AAF81280.1; -.

DR HSSP; P11215; 1BHQ.

DR GO; GO:0008305; C:integrin complex; IEA.

DR GO; GO:0007160; P:cell-matrix adhesion; IEA.

```
DR GO: 0007229; P: integrin-mediated signaling pathway; IEA.
DR InterPro: IPR000413; Integrin_alpha.
DR HSSP: P11215; 1BHQ.
DR InterPro: IPR000413; Integrin_alpha.
DR Pfam: PF01839; FG-GAP; 2.
DR Pfam: PF00357; Integrin_alpha; 1.
DR Pfam: PF00092; VWA; 1.
DR PRINTS: PRO1185; INTEGRINA.
DR PRINTS: PRO0453; VWFADOMAIN.
DR SMART: SM00191; Int_alpha; 5.
DR SMART: SM00327; VWA; 1.
DR PROSITE: PS00242; INTEGRIN_ALPHA; 1.
DR PROSITE: PS0234; VWEA; 1.
KW Cell adhesion; Integrin; Transmembrane.
SQ SEQUENCE 1151 AA; 126943 MW; 8F785695D4074CA5 CRC64;

Query Match
Best Local Similarity 72.6%; Score 669; DB 2; Length 1151;
Matches 130; Conservative 21; Mismatches 25; Indels 0; Gaps 0;

QY 1 CPQESDIAFLIDGSGSIIPHDPRMKFVSTVMEQLKSKTLFSLMOYSEFRHFTPK 60
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
144 CPQESNIAFLIDGSGSINTIDFQKMFVSTVMDQFQSKTLFSLMOYSDSFRTHFTN 203
QY 61 EFQNNPNRSLVKPIITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
204 DFKRNPDPKSHVRPIRQLNGRTKTAGIRKVVRELFQKNGARDNAAKILVITDGEKFG 263
QY 121 DPLGYEDVITPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPRDRHVFCQNNFE 176
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
264 DELNYEDVITPEAEAGIIRYVIGVGNFNAFKPQSRRELDTIASKPAGDHVFCQNDNE 319

RESULT 5
ITAD RAT STANDARD; PRT; 1161 AA.
AC Q9QV67.
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Integrin alpha-D precursor.
GN Name: Itgad;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RC STRAIN=Sprague-Dawley;
RA O'Brien M.M., VanderVieren M., Kilgannon P.D., Dietsch G.,
RA Gallatin W.M.;
RA "Cloning of rat alpha D, a novel beta 2 integrin.";
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC !- FUNCTION: Integrin alpha-D/beta-2 is a receptor for ICAM3 and
CC VCAM1. May play a role in the atherosclerotic process such as
CC clearing lipoproteins from plaques and in phagocytosis of blood-
CC borne pathogens, particulate matter, and senescent erythrocytes
CC from the blood (By similarity).
CC !- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-D
CC associates with beta-2 (By similarity).
CC !- SURCELLULAR LOCATION: Type I membrane protein (By similarity).
CC !- DOMAIN: The integrin I-domain (insert) is a VWEA domain. Integrins
CC with I-domains do not undergo protease cleavage.
CC !- SIMILARITY: Belongs to the integrin alpha chain family.
CC !- SIMILARITY: Contains 7 FG-GAP repeats.
CC !- SIMILARITY: Contains 1 VWEA domain.
CC
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CC EMBL; AF021334; AAF21241.1; -.
DR HSSP: P11215; 1BHQ.
DR InterPro: IPR000413; Integrin_alpha.
DR InterPro: IPR000413; Integrin_alpha.
DR Pfam: PF01839; FG-GAP; 3.
DR Pfam: PF00357; Integrin_alpha; 1.
DR Pfam: PF00092; VWA; 1.
DR PRINTS: PRO1185; INTEGRINA.
DR PRINTS: PRO0453; VWFADOMAIN.
DR SMART: SM00191; Int_alpha; 5.
DR SMART: SM00327; VWA; 1.
DR PROSITE: PS00242; INTEGRIN_ALPHA; 1.
DR PROSITE: PS0234; VWEA; 1.
KW Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
KW Repeat; Signal; Transmembrane.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 1161 Integrin alpha-D.
FT DOMAIN 20 1100 Extracellular (Potential).
FT TRANSMEM 1101 1121 Potential.
FT DOMAIN 1122 1161 Cytoplasmic (Potential).
FT REPEAT 34 87 FG-GAP 1.
FT REPEAT 88 2 FG-GAP 2.
FT REPEAT 152 334 VWEA.
FT REPEAT 352 402 FG-GAP 3.
FT REPEAT 403 454 FG-GAP 4.
FT REPEAT 456 517 FG-GAP 5.
FT REPEAT 519 577 FG-GAP 6.
FT REPEAT 582 634 FG-GAP 7.
FT CA_BIND 467 475 Potential.
FT CA_BIND 531 539 Potential.
FT CA_BIND 594 602 Potential.
FT SITE 1126 1130 GPFKR motif.
FT DISULFID 69 76 By similarity.
FT DISULFID 108 126 By similarity.
FT DISULFID 656 711 By similarity.
FT DISULFID 769 775 By similarity.
FT DISULFID 845 860 By similarity.
FT DISULFID 993 1017 By similarity.
FT DISULFID 1022 1027 By similarity.
FT CARBOHYD 61 61 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 89 89 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 245 245 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 393 393 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 696 696 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 734 734 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 784 784 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 907 907 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 936 936 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1045 1045 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 1161 AA; 126600 MW; 2258491A984A705E CRC64;

Query Match
Best Local Similarity 59.7%; Score 550; DB 1; Length 1161;
Matches 106; Conservative 27; Mismatches 42; Indels 0; Gaps 0;

QY 1 CPQESDIAFLIDGSGSIIPHDPRMKFVSTVMEQLKSKTLFSLMOYSEFRHFTPK 60
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
146 CDRQEMDIAFLIDGSGSINQDRDFAQMDKDFVKGALMGEPASTLFLSLMQSLNLIKTHFTT 205
QY 61 EFQNNPNRSLVKPIITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
206 EFKNLDLPQSLVDPIVQLQGLTYTATGIRTVMEELFHSKNGSKSAKILLVITDQKYR 265
QY 121 DPLGYEDVITPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPRDRHVFCQNNFE 175
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
266 DPLEYSDVIPADKAGIIRYVIGVGNFNAFKPQSRRELDTIASKPAGDHVFCQNNFE 320

RESULT 6
ITAD HUMAN
ID ITAD_HUMAN STANDARD; PRT; 1162 AA.
AC Q13349; Q15575; Q15576;
```

16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-JUN-2004 (Rel. 44, Last annotation update)
Integrin alpha-D precursor (Leukointegrin alpha D) (CD11d) (ADB2).
Name=ITGAD;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Splice;
RX MEDLINE=96111956; PubMed=8777714;
RA Van der Vliet M., Le Trong H., Wood C.L., Moore P.F., St John T.,
ST Staunton D.E., Gallatin W.M.;
RT "A novel leukointegrin, alpha d beta 2, binds preferentially to ICAM-
3.";
RL J. Biol. Chem. 275:8959-8969(2000).
RN [2]
RP SEQUENCE OF 1-235 FROM N.A.
RX MEDLINE=20187620; PubMed=10722744;
RA Noti J.D., Johnson A.K., Dillon J.D.;
RT "Structural and functional characterization of the leukocyte integrin
gene CD11d. Essential role of Sp1 and Sp3.";
RL J. Biol. Chem. 275:8959-8969(2000).
RN [3]
RP SEQUENCE OF 467-537; 571-602; 633-666; 788-834 AND 910-1125 FROM N.A.
RX MEDLINE=96257236; PubMed=8666289;
RA Wong D.A., Davis E.M., LeBeau M., Springer T.A.;
RT "Cloning and chromosomal localization of a novel gene encoding a human
beta 2-integrin alpha subunit.";
RL Gene 171:291-294(1996).
RN [4]
RP INTERACTION WITH VCAM1.
RX MEDLINE=99059842; PubMed=9841932;
RA Grayson M.H., Van der Vliet M., Sterbinsky S.A., Michael Gallatin W.,
Hoffman P.A., Staunton D.E., Bochner B.S.;
RT "alpha2beta2 integrin is expressed on human eosinophils and functions
as an alternative ligand for vascular cell adhesion molecule 1 (VCAM-
1)." ;
RL J. Exp. Med. 188:2187-2191(1998).
RN [5]
RP INTERACTION WITH VCAM1.
RX MEDLINE=99370002; PubMed=10438935;
RA Van der Vliet M., Crowe D.T., Hoekstra D., Vazeux R., Hoffman P.A.,
Grayson M.H., Bochner B.S., Gallatin W.M., Staunton D.E.;
RT "The leukocyte integrin alpha D beta 2 binds VCAM-1: evidence for a
binding interface between I domain and VCAM-1." ;
RL J. Immunol. 163:1984-1990(1999).
CC -!- FUNCTION: Integrin alpha-D/beta-2 is a receptor for ICAM3 and
clearing lipoproteins from plaques and in phagocytosis of blood-
borne pathogens, particulate matter, and senescent erythrocytes
from the blood.
CC -!- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-D
associates with beta-2.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed moderately on myelomonocytic cell
lines and subsets of peripheral blood leukocytes and strongly on
tissue-specialized cells, including macrophages foam cells within
atherosclerotic plaques, and on splenic red pulp macrophages.
CC -!- DOMAIN: The integrin I-domain (inset) is a VWFA domain. Integrins
with I-domains do not undergo protease cleavage.
CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
CC -!- SIMILARITY: Contains 7 FG-GAP repeats.
CC -!- SIMILARITY: Contains 1 VWFA domain.

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CC CC EMBL; U37028; AAB38547.1; --
CC DR EMBL; U40274; AAB60634.1; --
CC DR EMBL; U40275; AAB60635.1; --
CC DR EMBL; U40276; AAB60636.1; --
CC DR EMBL; U40277; AAB60637.1; --
CC DR EMBL; U40279; AAB60638.1; --
CC DR EMBL; U40278; AAB60638.1; JOINED.
CC DR EMBL; AF187881; AAF62875.1; --
CC DR HSSP; FI1215; 1BHQ.
CC DR Genew; HGNC:6146; ITGAD.
CC DR MIM; 602453; --
CC GO; GO:0008305; C:integrin complex; TAS.
CC GO; GO:0016337; P:cell-cell adhesion; NAS.
CC GO; GO:0007160; P:cell-matrix adhesion; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC DR InterPro; IPR000413; Integrin_alpha.
CC DR InterPro; IPR02035; VWFA.
CC Pfam; PF01839; FG-GAP; 3.
CC Pfam; PF00357; Integrin_alpha; 1.
CC Pfam; PF00092; VWFA; 1.
CC PRINTS; PR01185; INTEGRINA.
CC PRINTS; PR00453; VWFADOMAIN.
CC SMART; SM00191; Int_alpha; 5.
CC SMART; SM00327; VWFA; 1.
CC PROSITE; PS00242; INTEGRIN_ALPHA; 1.
CC PROSITE; PS0234; VWFA; 1.
CC Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
KW Repeat; Signal; Transmembrane.
FT SIGNAL 1 17 Potential.
FT CHAIN 18 1162 Integrin alpha-D.
FT DOMAIN 18 1100 Extracellular (Potential).
FT TRANSMEM 1101 1121 Potential.
FT DOMAIN 1122 1162 Cytoplasmic (Potential).
FT REPEAT 32 85 FG-GAP 1.
FT REPEAT 86 85 FG-GAP 2.
FT DOMAIN 150 332 VWFA.
FT REPEAT 350 400 FG-GAP 3.
FT REPEAT 401 452 FG-GAP 4.
FT REPEAT 454 516 FG-GAP 5.
FT REPEAT 518 576 FG-GAP 6.
FT REPEAT 581 633 FG-GAP 7.
FT CA_BIND 465 473 Potential.
FT CA_BIND 530 538 Potential.
FT CA_BIND 593 601 Potential.
FT SITE 1127 1131 GFFKR motif.
FT DISULFID 67 74 By similarity.
FT DISULFID 106 124 By similarity.
FT DISULFID 655 710 By similarity.
FT DISULFID 769 775 By similarity.
FT DISULFID 846 861 By similarity.
FT DISULFID 994 1018 By similarity.
FT DISULFID 1023 1028 By similarity.
FT CARBOHYD 59 59 N-linked (GlcNAc...)
FT CARBOHYD 87 87 N-linked (GlcNAc...)
FT CARBOHYD 99 99 N-linked (GlcNAc...)
FT CARBOHYD 391 391 N-linked (GlcNAc...)
FT CARBOHYD 691 691 N-linked (GlcNAc...)
FT CARBOHYD 733 733 N-linked (GlcNAc...)
FT CARBOHYD 873 873 N-linked (GlcNAc...)
FT CARBOHYD 957 957 N-linked (GlcNAc...)
FT CARBOHYD 1046 1046 N-linked (GlcNAc...)
FT CONFLICT 500 500 Missing (in Ref. 2).
FT CONFLICT 515 518 GHPW -> ATP (in Ref. 2).
FT CONFLICT 825 825 L -> V (in Ref. 2).
FT CONFLICT 984 984 V -> A (in Ref. 2).
SQ SEQUENCE 1162 AA; 126885 MW; F296A1A35455D77D CRC64;
Query Match 59.1%; Score 545; DB 1; Length 1162;
Best Local Similarity 60.0%; Pred. No. 7.5e-37;
Matches 105; Conservative 29; Mismatches 41; Indels 0; Gaps 0;


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QY 1 CQEDSDIAFLDGSIIIPHRKKEFVSTVMEQLKKSKTLFSLMQYSEBFRIHPTFK 60
DB 144 CPEHMDIVFLDGGSIDQDNFNQMGFVQVAMGQFEGDTLFLALMQYSLNLLKIHFTFT 203
QY 61 BFQNNPRLSKVPTQLLGRHTTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 204 QRTSPSQSLVDPVQLKGLTFTAGILTVTQLFHHKNGARKNAFKILVITDGEKRYK 263
QY 121 DPLGVEDVPEADREGVIRYVIGVDGDAFRSEKSRQELNTIASKPPRDHVFQCNFF 175
DB 264 DPLEYSDVIPAQKAGIIRIYAGVGHAFQGPARTARQELNTIASSAPPQDHVFKVDNF 318

RESULT 7
Q63001 PRELIMINARY; PRT; 205 AA.
ID Q63001
AC Q63001;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Integrin alpha-M (Fragment).
GN Name=Itgam;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN NCBI_TaxID=10116;
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar Kyoto;
RA Nabika T., Ito T., Kitada H., Serikawa T., Mahimo T., Soubrier F.,
RA Jullier C., Maeda J., Yamori Y., Nara Y.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U59801; AA03226.1; -
DR GO; GO:000729; P:intrigued-mediated signaling pathway; IEA.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF00092; VWA; 1.
DR PRINTS; PRO0453; VWFADOMAIN.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS0234; VWPA; 1.
KW Integrin.
FT NON_TER 1
FT NON_TER 205
SQ SEQUENCE 205 AA; 22922 MW; C8C2D9395008DA36 CRC64;

Query Match 57.8%; Score 533; DB 2; Length 205;
Best Local Similarity 74.1%; Pred. No. 1,1e-36;
Matches 109; Conservative 14; Mismatches 24; Indels 0; Gaps 0;

QY 30 VSTVMEQLKKSKTLFSLMQYSEBFRIHPTFKFQNNPRLSKVPTQLLGRHTTATGIR 89
DB 1 VSTVMEQFQSKTLFSLMQYSEBFRTFTFNFKENPDKSHVRPIQLNGRTKTASGIR 60
QY 90 KVVRELFNITNGARKNAFKILVITDGEKFGDPLGVEDVPEADREGVIRYVIGVDAPR 149
DB 61 KVVRELFQKINGARNAFKILVITDGEKFGDPLGVEDVPEAEAGIIRYVIGVXNAPH 120
QY 150 SEKSRQELNTIASKPPRDHVFQCNFFE 176
DB 121 KPQSRRELDITASKPAGDHVFDVDFE 147

RESULT 8
ITAX HUMAN
ID ITAX HUMAN STANDARD; PRT; 1163 AA.
AC P20702; O81VA6;
DT 01-FEB-1991 (Rel. 17, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Integrin alpha-X precursor (Leukocyte adhesion glycoprotein p150,95
DE alpha chain) (Leukocyte adhesion receptor p150,95) (CD11c) (Lew M5).
GN Name=ITGAX; Synonyms=CD11c;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN NCBI_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=88166645; PubMed=3327687;
RA Corbi A.L., Miller L.J., O'Connor K., Larson R.S., Springer T.A.;
RT "cDNA cloning and complete primary structure of the alpha subunit of a
RT leukocyte adhesion glycoprotein, p150,95."
RL EMBO J. 6:4023-4028(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90153906; PubMed=2303426;
RA Corbi A.L., Garcia-Aguilar J., Springer T.A.;
RT "Genomic structure of an integrin alpha subunit, the leukocyte p150,95
RT molecule."
RL J. Biol. Chem. 265:2782-2788(1990).
RN [3]
RP ERRATUM.
RA Corbi A.L., Garcia-Aguilar J., Springer T.A.;
RL J. Biol. Chem. 265:12750-12751(1990).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=22388957; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 20-43.
RX MEDLINE=87167596; PubMed=3549901;
RA Miller L.J., Wiebe M., Springer T.A.;
RT "Purification and alpha subunit N-terminal sequences of human Mac-1
RT and p150,95 leukocyte adhesion proteins."
RL J. Immunol. 138:2381-2383(1987).
CC -!- FUNCTION: Integrin alpha-X/beta-2 is a receptor for fibrinogen. It
CC recognizes the sequence G-P-R in fibrinogen. It mediates cell-cell
CC interaction during inflammatory responses. It is especially
CC important in monocyte adhesion and chemotaxis.
CC -!- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-X
CC associates with beta-2.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Predominantly expressed in monocytes and
CC granulocytes.
CC -!- DOMAIN: The integrin I-domain (insert) is a VWA domain. Integrins
CC with I-domains do not undergo protease cleavage.
CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
CC -!- SIMILARITY: Contains 7 FG-GAP repeats.
CC -!- SIMILARITY: Contains 1 VWA domain.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide Cdlc entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdlc.htm".
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  EMBL; M81695; AAA59180.1; -
CC  EMBL; M29165; -; NOT ANNOTATED CDS.
CC  EMBL; M29487; AAA51620.1; ALT_SEQ.
CC  EMBL; M29482; AAA51620.1; JOINED.
CC  EMBL; M29483; AAA51620.1; JOINED.
CC  EMBL; M29484; AAA51620.1; JOINED.
CC  EMBL; M29485; AAA51620.1; JOINED.
CC  EMBL; M29486; AAA51620.1; JOINED.
CC  EMBL; BC038237; AAH38237.1; -.
CC  PIR; A36584; RWHUIC.
CC  PDB; 1N3Y; X-ray; A=141-338.
CC  Genew; HGNC:6152; ITGAX.
CC  MIM; 151510; -.
CC  GO; GO:0008305; C:integrin complex; TAS.
CC  GO; GO:0004872; F:receptor activity; TAS.
CC  GO; GO:0007155; P:cell adhesion; TAS.
CC  GO; GO:0009887; P:organogenesis; TAS.
CC  InterPro; IPR000413; Integrin_alpha.
CC  InterPro; IPR002035; VWF_A.
CC  Pfam; PF01839; FG-GAP_3.
CC  Pfam; PF00357; Integrin_alpha; 1.
CC  Pfam; PF00092; VWA; 1.
CC  PRINTS; PR01185; INTEGRINA.
CC  PRINTS; PR00453; VWFADOMAIN.
CC  SMART; SM00191; Int_alpha; 5.
CC  SMART; SM00327; VWA_1.
CC  PROSITE; PS00242; INTEGRIN_ALPHA; 1.
CC  PROSITE; PS0234; VWFA; 1.
CC  3D-structure; Calcium; Cell adhesion; Direct protein sequencing;
KW Glycoprotein; Integrin; Magnesium; Polymorphism; Receptor; Repeat;
KW Signal; Transmembrane.
FT SIGNAL 1 19
FT CHAIN 20 1163
FT DOMAIN 20 1107 Integrin alpha-X.
FT TRANSMEM 1108 1128 Extracellular (Potential).
FT REPEAT 34 87 Potential.
FT REPEAT 88 ? Cytoplasmic (Potential).
FT DOMAIN 165 351 FG-GAP 1.
FT REPEAT ? 401 FG-GAP 2.
FT REPEAT 402 453 VWFA.
FT REPEAT 455 517 FG-GAP 3.
FT REPEAT 518 576 FG-GAP 4.
FT REPEAT 581 633 FG-GAP 5.
FT CA_BIND 456 474 FG-GAP 6.
FT CA_BIND 530 538 FG-GAP 7.
FT SITE 593 601 Potential.
FT SITE 1131 1135 Potential.
FT DISULFID 69 76 GFPR motif.
FT DISULFID 108 126 By similarity.
FT DISULFID 655 712 By similarity.
FT DISULFID 771 777 By similarity.
FT DISULFID 848 863 By similarity.
FT DISULFID 998 1022 By similarity.
FT DISULFID 1027 1032 By similarity.
FT CARBOHYD 61 61 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 89 89 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 392 392 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 697 697 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 735 735 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 899 899 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 939 939 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1050 1050 N-linked (GlcNAc...) (Potential).
FT VARIANT 48 48 W -> R (in dbSNP:11574633).
FT CONFLICT 209 209 /FTID=VAR_018672.
FT CONFLICT 251 251 T -> S (in Ref. 4).
FT CONFLICT 469 469 T -> A (in Ref. 4).
FT CONFLICT 490 490 T -> S (in Ref. 4).
FT CONFLICT 547 547 G -> A (in Ref. 2).
FT CONFLICT 547 547 E -> K (in Ref. 4).

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FT CONFLICT 756 756 D -> L (in Ref. 1).
FT CONFLICT 819 819 I -> V (in Ref. 4).
FT CONFLICT 1163 1163 SEK -> TPHYPQDNV (in Ref. 4).
FT STRAND 150 157
FT TURN 160 161
FT HELIX 164 178
FT TURN 179 180
FT TURN 183 185
FT STRAND 186 193
FT STRAND 197 201
FT HELIX 203 208
FT TURN 212 216
FT TURN 217 218
FT STRAND 226 226
FT HELIX 228 236
FT TURN 237 240
FT HELIX 242 244
FT TURN 245 245
FT TURN 248 249
FT STRAND 251 258
FT STRAND 263 263
FT HELIX 269 278
FT TURN 279 280
FT STRAND 282 288
FT HELIX 290 293
FT TURN 296 297
FT HELIX 298 304
FT HELIX 310 312
FT STRAND 313 316
FT HELIX 319 325
FT HELIX 326 334
FT TURN 335 335
SQ SEQUENCE 1163 AA; 127886 MW; 83658A13B5C5DE8F CRC64;

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Query Match 52.7%; Score 486; DB 1; Length 1163;

Best Local Similarity 53.4%; Pred. No. 6.6e-32;
Matches 94; Conservative 33; Mismatches 49; Indels 0; Gaps 0;

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QY 1 CPQDSDFIAFLDGGSGSIIPHDFFRMKEFYSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60
Db 145 CPQEQDIVLIDGSGSISSRNFMNFVRAVTSQFQPSQSLMQFSNKFQHTFTE 204
QY 61 EFQNNPNRSLVKPITQLLGRTHGTATGIRKVVRELFNITGARKNAFKILVITDGEKFG 120
Db 205 EFRRTSNPLSLASVHQLQGFTYTATAIQNVVHFLPHASYGARDATKILIVITDGKKEG 264
QY 121 DPLGYEDVIPADREGVIRVIGVDAPRSEKSRQELNTASKPRDHVFCNNFE 176
Db 265 DSLDYKDVIPWADAAGIIRYAIGVGLAFQNNRNSWKELNDIASKPSQBHFVKVEDFD 320

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RESULT 9

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Q6KAS4 PRELIMINARY; PRT; 1188 AA.
ID Q6KAS4
AC Q6KAS4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE MFLJ00114 protein (Fragment).
GN Name=mLJ00114;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Soga Y., Kitamura H., Nakagawa T., Nagase T., Ohara O., Koga H.;
RT "Prediction of the Coding Sequences of Mouse Homologues of FLJ Genes:
RT The Complete Nucleotide Sequences of 110 Mouse FLJ-Homologous cDNAs
RT Identified by Screening of Terminal Sequences of cDNA Clones Randomly
RT Sampled from Size-Fractionated Libraries.";
RL DNA Res. 11:167-180 (2004).

```

CC -I- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -I- SIMILARITY: Belongs to the integrin alpha chain family.
DR EMBL; AK131133; BAD21383.1; -
DR GO; GO:0009897; C:external side of plasma membrane; IDA.
DR InterPro; IPR000413; Integrin_alpha.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF01839; EG-GAP; 3.
DR Pfam; PF00357; Integrin_alpha; 1.
DR Pfam; PF00092; VWA; 1.
DR PRINTS; PR01185; INTEGRIN.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00191; Int_alpha; 5.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS00242; INTEGRIN_ALPHA; UNKNOWN_1.
DR PROSITE; PS0234; VWF_A; 1.
KW Cell adhesion; Integrin; Transmembrane.
KW NON_TER 1
FT NON_TER 1
SQ SEQUENCE 1188 AA; 131248 MW; B8D93107BDBB4178 CRC64;

Query Match 52.4%; Score 483; DB 2; Length 1188;
Best Local Similarity 52.8%; Pred. No. 1.2e-31;
Matches 93; Conservative 30; Mismatches 53; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKXTLFSLMQYSEFRIHFTFK 60
DB ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
165 CPKQDQDIVFLIDGSGSISSTDFEKMILDFVKAVMSQLQRPSTRFSLMQFSDFYRVHFTFN 224

QY 61 EFQNNPNRSLVKPIITOLLGTHRTATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
DB ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
225 NFISSPFLSDSVRLQGYTYTASAIKHVITELFTTQSGARQDATKVLIVTDGRKQG 284

QY 121 DPLGYEDVIPEDAREGVIRVIGVDAPFRSEKRSQELNTIASKPPRDHVFQCNFFE 176
DB ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
285 DNLSDSVIPMAEASIIRYAIGVGKAFYNEHSHKQELKAIASMPSEHYVFSVENFD 340

RESULT 10
BAD21383 PRELIMINARY; PRT; 1188 AA.
ID ID BAD21383
AC BAD21383;
DT 01-JUN-2004 (TrEMBLrel. 27, Created)
DT 01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DE 01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE MFLJ00114 protein (fragment).
OS MFLJ00114.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Suga Y., Kitamura H., Nakagawa T., Nagase T., Ohara O., Koga H.;
RT "Prediction of the Coding Sequences of Mouse Homologues of FLJ Gene:
RT The Complete Nucleotide Sequences of 110 Mouse FLJ-homologous cDNAs
RT Identified by Screening of Terminal sequences of cDNA Clones Randomly
RT Sampled from Size-Fractionated Libraries.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK131133; BAD21383.1; -
DR NON_TER 1
FT NON_TER 1
SQ SEQUENCE 1188 AA; 131248 MW; B8D93107BDBB4178 CRC64;

Query Match 52.4%; Score 483; DB 2; Length 1188;
Best Local Similarity 52.8%; Pred. No. 1.2e-31;
Matches 93; Conservative 30; Mismatches 53; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKXTLFSLMQYSEFRIHFTFK 60
DB ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
165 CPKQDQDIVFLIDGSGSISSTDFEKMILDFVKAVMSQLQRPSTRFSLMQFSDFYRVHFTFN 224

QY 61 EFQNNPNRSLVKPIITOLLGTHRTATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
DB ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
225 NFISSPFLSDSVRLQGYTYTASAIKHVITELFTTQSGARQDATKVLIVTDGRKQG 284

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FT REPEAT ? 402 FG-GAP 3.
FT REPEAT 403 454 FG-GAP 4.
FT REPEAT 456 518 FG-GAP 5.
FT REPEAT 519 577 FG-GAP 6.
FT REPEAT 582 634 FG-GAP 7.
FT CA_BIND 467 475 Potential.
FT CA_BIND 531 539 Potential.
FT CA_BIND 594 602 Potential.
FT SITE 1140 1144 GFPCR motif.
FT DISULFID 69 76 By similarity.
FT DISULFID 108 126 By similarity.
FT DISULFID 656 711 By similarity.
FT DISULFID 770 776 By similarity.
FT DISULFID 858 873 By similarity.
FT DISULFID 1007 1031 By similarity.
FT DISULFID 1036 1041 By similarity.
FT CARBOHYD 89 89 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 267 287 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 393 393 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 734 734 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 949 949 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1059 1059 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1084 1084 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 1169 AA; 129150 MW; C616412033C219A6 CRC64;

Query Match 52.3%; Score 482; DB 1; Length 1169;
Best Local Similarity 52.8%; Pred. No. 1.4e-31;
Matches 93; Conservative 30; Mismatches 53; Indels 0; Gaps 0;

QY 1 CPQSDSIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKKSKTLFLSMQYSEEFRIHFTFK 60
Db 146 CPKQDQIVFLIDGSGSISSTDFEKLDFVKAVMSQLQRPSTFRSLMQFSDFYRVHFTFN 205

QY 61 EFQNNPNRSLVKPIITQLGRHTHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
Db 206 NFISTSSPLSLGSLVRLQGRGYTYTASAKHVITELFTTQSGARQDATKVLIVITDGRKQG 265

QY 121 DPLGYEDVPEADREGVIRYVIGVDGAFRSEKSRQELNTIASKPPRDHVFQCNNEP 176
Db 266 DNLSDYSVIPMAEASIIIRYAGVGNKAFVNEHSKQELKAIASMPHSHEVVFVSENF 321

RESULT 12
QPG66
ID Q6PG66 PRELIMINARY; PRT; 304 AA.
AC Q6PG66
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Integrin alpha X.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129; TISSUE=Mammary tumor. Brca1-/fl;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

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RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129; TISSUE=Mammary tumor. Brca1-/fl;
RA Strausberg R.;
RL Submitted (AUG-2003) to the ENBL/GenBank/DBJ databases.
DR EMBL; EC057200; AAH57200.1; -.
DR GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF00092; VWA; 1.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS02334; VWF_A; 1.
KW Integrin.
SQ SEQUENCE 304 AA; 33404 MW; EC52F3EA48FA068D CRC64;

Query Match 44.3%; Score 408; DB 2; Length 304;
Best Local Similarity 53.3%; Pred. No. 5.1e-26;
Matches 80; Conservative 25; Mismatches 43; Indels 2; Gaps 1;

QY 1 CPQSDSIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKKSKTLFLSMQYSEEFRIHFTFK 60
Db 146 CPKQDQIVFLIDGSGSISSTDFEKLDFVKAVMSQLQRPSTFRSLMQFSDFYRVHFTFN 205

QY 61 EFQNNPNRSLVKPIITQLGRHTHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
Db 206 NFISTSSPLSLGSLVRLQGRGYTYTASAKHVITELFTTQSGARQDATKVLIVITDGRKQG 265

QY 121 DPLGYEDVPEADREGVIRYVIGVG--DAF 148
Db 266 DNLSDYSVIPMAEASIIIRYAGVGNKQGF 295

RESULT 13
AAH57200
ID AAH57200 PRELIMINARY; PRT; 304 AA.
AC AAH57200;
DT 02-MAR-2004 (TReMBLrel. 27, Created)
DT 02-MAR-2004 (TReMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TReMBLrel. 27, Last annotation update)
DE Integrin alpha X.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129; TISSUE=Mammary tumor. Brca1-/fl;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

```

```

[2]
RP SEQUENCE FROM N.A.
RC STRAIN=129; TISSUE=Mammary tumor. Brca1-/fl;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC057200; AAH57200.1; -.
KW Integrin.
SQ SEQUENCE 304 AA; 33404 MW; EC52F3EA48FA068D CRC64;

Query Match 44.3%; Score 408; DB 2; Length 304;
Best Local Similarity 53.3%; Pred. No. 5.1e-26;
Matches 80; Conservative 25; Mismatches 43; Indels 2; Gaps 1;

QY 1 CPOEDSDIAFLIDSGSIIIPHDFRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 60
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DQ 146 CPKQDQIVFLIDSGSISSTDFKMLDFKAVMSQLQSPRFSLSMQPSDYFRVHFTFN 205
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 EFQNNPNRSLVKPTQLLGRTHATGIRKVVRELFNTNGARKNAFKLVITDGEKFG 120
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DQ 206 NFISTSPSLSDSVRQURGYTYTASAKHVITELFTTQSGARQDATKVLIVITDGRKQG 265
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 DPLGYEDVIPADREGVIRYVIGVG--DAF 148
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DQ 266 DNLSDSVIPMAEASIIIRYAGVGHKQCF 295
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 14
Q9WUF8 PRELIMINARY; PRT; 895 AA.
AC Q9WUF8;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Itgae protein (Fragment).
GN Name=Itgae;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RA Schoen M.P., Arya A., Murphy E.A., Adams C.M., Strauch U.G.,
RA Agace W.W., Marsal J., Donohue J.P., Her H., Beler D.R., Olson S.,
RA Lefrancois L., Brenner M.B., Grusby M.J., Parker C.M.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
DR EMBL; AF133085; AAD30063.1; JOINED.
DR EMBL; AF133070; AAD30063.1; JOINED.
DR EMBL; AF133071; AAD30063.1; JOINED.
DR EMBL; AF133072; AAD30063.1; JOINED.
DR EMBL; AF133073; AAD30063.1; JOINED.
DR EMBL; AF133074; AAD30063.1; JOINED.
DR EMBL; AF133075; AAD30063.1; JOINED.
DR EMBL; AF133076; AAD30063.1; JOINED.
DR EMBL; AF133077; AAD30063.1; JOINED.
DR EMBL; AF133078; AAD30063.1; JOINED.
DR EMBL; AF133079; AAD30063.1; JOINED.
DR EMBL; AF133080; AAD30063.1; JOINED.
DR EMBL; AF133081; AAD30063.1; JOINED.
DR EMBL; AF133082; AAD30063.1; JOINED.
DR EMBL; AF133083; AAD30063.1; JOINED.
DR EMBL; AF133084; AAD30063.1; JOINED.
DR GO; GO:0008305; C-integrin complex; IEA.
DR GO; GO:0007160; P-cell-matrix adhesion; IEA.
DR InterPro; IPR000413; Integrin_alpha.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF01839; FG-GAP; 3.
DR Pfam; PF00092; VWA; 1.
DR PRINTS; PR01185; INTEGRINA.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00191; Int_alpha; 4.
DR SMART; SM00327; VWA; 1.

DR PROSITE; PS50234; VWFA; 1.
KW Cell adhesion; Integrin; Transmembrane.
FT NON_TER 1
FT NON_TER 895
SQ SEQUENCE 895 AA; 98265 MW; BE6EA14A754ADA1E CRC64;

Query Match 34.9%; Score 322; DB 2; Length 895;
Best Local Similarity 38.3%; Pred. No. 2.7e-18;
Matches 67; Conservative 40; Mismatches 66; Indels 2; Gaps 1;

QY 3 QEDSDIAFLIDSGSIIIPHDFRMKEFVSTVMEQL--KSKTLFSLMOYSEEFRIHFTFK 60
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DQ 178 EDGTIAIIVLDGSGSIEPSDFQAKNFISTWRNFEKCFECNFALVQYGVITQTEFDLQ 237
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 EFQNNPNRSLVKPTQLLGRTHATGIRKVVRELFNTNGARKNAFKLVITDGEKFG 120
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DQ 238 ESRDINASLAKVQSIVQVKEVKTASAMQHVLDNIFIPSRGSRKKALKVMVLTGDDIFG 297
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 DPLGYEDVIPADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNPF 175
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DQ 298 DPLNLTTVINSKMGVVRFAIGVGDAFKNNNTYRELKLIASDPKEAHTFKVTNY 352
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 15
Q8BS01 PRELIMINARY; PRT; 1038 AA.
AC Q8BS01;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Mus musculus adult male aorta and vein cDNA, RIKEN full-length
DE enriched library, clone:AS3055J10 product:integrin, alpha E,
DE epithelial-associated, full insert sequence.
GN Name=Itgae;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX MEDLINE=92729253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX The FANTOM Consortium.
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX MEDLINE=20530913; PubMed=11076861;
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2005, 14:59:41 ; Search time 33.0928 Seconds
(without alignments)
1918.696 Million cell updates/sec

Title: RWHULB-C_COPY_144_320
Perfect score: 922
Sequence: 1 CPQESDIAFLDGSIIIP.....NTIAKPRDRHVQCNFEC 177

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	912	98.9	177	5	Aau76866 Human int
2	903	97.9	187	2	Aay21991 Human com
3	903	97.9	1152	8	Adm99589 Human int
4	903	97.9	1152	8	Adp12435 Protein e
5	903	97.9	1153	2	Aar04136 Alpha sub
6	903	97.9	1153	2	Aaw65090 Human Bet
7	903	97.9	1153	3	Aab07360 Human CDI
8	903	97.9	1153	5	Aau80252 Human int
9	903	97.9	1153	5	Abg61469 Human Bet
10	903	97.9	1153	5	Aa014428 Integrin
11	903	97.9	1153	7	Add25615 Binding d
12	894	97.0	177	5	Aau76865 Human int
13	893	96.9	191	5	Aau76856 Human int
14	893	96.9	191	5	Aau76847 Human int
15	871	94.5	216	4	Aab66766 Amino aci
16	871	94.5	435	2	Aar77461 GST-I-dom
17	863	74.1	199	5	Abb78072 Marine I-
18	559	60.6	413	2	Aaw23065 Rabbit be
19	559	60.6	413	2	Aaw65107 Rabbit al
20	559	60.6	413	2	Aaw72839 Rabbit al
21	559	60.6	413	2	Aaw73348 Rabbit al
22	559	60.6	413	3	Aab07377 Rabbit al
23	557	60.4	413	5	Abg61486 Rabbit Be
24	550	59.7	1151	2	Aaw23059 Rat beta
25	550	59.7	1151	2	Aaw60001 Rat alpha

26	550	59.7	1151	2	AAW65101	Aaw65101 Rat beta-
27	550	59.7	1151	2	AAW72834	Aaw72834 Rat alpha
28	550	59.7	1151	2	AAW73344	Aaw73344 Rat alpha
29	550	59.7	1151	3	AAW07371	Aab07371 Rat alpha
30	550	59.7	1151	5	ABG61480	Abg61480 Rat Beta2
31	550	59.7	1161	2	AAW78169	Aar78169 Rat alpha
32	550	59.7	1161	2	AAW23062	Aaw23062 Rat beta
33	550	59.7	1161	2	AAW60004	Aaw60004 Rat alpha
34	550	59.7	1161	2	AAW65104	Aaw65104 Rat beta-
35	550	59.7	1161	2	AAW72824	Aaw72824 Rat alpha
36	550	59.7	1161	2	AAW73345	Aaw73345 Rat alpha
37	550	59.7	1161	3	AAW07374	AAW07374 Rat alpha
38	550	59.7	1161	5	ABG61483	ABG61483 Rat Beta2
39	549	59.5	1151	2	AAW78179	Aar78179 Rat alpha
40	545	59.1	1161	2	AAW78166	Aar78166 Human bet
41	545	59.1	1161	2	AAW23049	Aaw23049 Human bet
42	545	59.1	1161	2	AAW23064	Aaw23064 Human bet
43	545	59.1	1161	2	AAW57491	Aaw57491 Human bet
44	545	59.1	1161	2	AAW65106	Aaw65106 Human Bet
45	545	59.1	1161	2	AAW65089	Aaw65089 Human Bet

ALIGNMENTS

RESULT 1
AAU76866
ID AAU76866 standard; protein; 177 AA.
XX
AC AAU76866;
XX
DT 21-MAY-2002 (first entry)
XX
DE Human integrin alpha subunit CD11b deletion variant A domain #2.
XX
KW Human; integrin alpha subunit; A domain; CD11b; integrin beta subunit;
KW A-like domain; inflammatory disorder; skeletal muscle injury; restenosis;
KW ischaemia-reperfusion injury; immune complex; parasitic disease; mutant;
KW antinflammatory; vasotropic; antiparasitic; vulnerary; gene therapy;
KW murein.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 172 /note= "Wild-type Val substituted by Cys"
FT Misc-difference 177 /note= "Wild-type Ala substituted by Cys"
FT
FT WO200209737-A1.
XX
PD 07-FEB-2002.
XX
XX 31-JUL-2001; 2001WO-US023957.
XX
XX 31-JUL-2000; 2000US-0221950P.
XX 11-JAN-2001; 2001US-00758493.
XX 13-MAR-2001; 2001US-00805354.
XX (GEO) GEN HOSPITAL CORP.
XX
XX Arnaout AM, Li R, Xiong J;
XX WPI; 2002-188687/24..
XX
XX Novel high affinity integrin polypeptide useful for treating restenosis
XX and parasitic diseases, comprises all or part of variant integrin alpha
XX subunit A domain or variant integrin beta subunit A-like domain.
XX Claim 21; Page; 55pp; English.
XX The invention relates to a high affinity integrin polypeptide comprising

CC all or part of a variant integrin alpha subunit A domain or a variant
 CC integrin beta subunit A-like domain. The polypeptide, preferably the
 CC CD11b alpha subunit A domain, where I at residue 332 has been replaced by
 CC G or A, F at residue 313 and A at residue 320 have been replaced by C, or
 CC V at residue 315 and A at residue 320 have been replaced by C, is useful
 CC for determining if a test compound is a candidate compound for binding to
 CC CD11b or for treating an inflammatory disorder, by contacting a test
 CC compound with the polypeptide and determining if the test compound binds
 CC to the polypeptide. The integrin subunits are useful for reducing
 CC skeletal muscle injury, for treating disorders caused by ischaemia-
 CC reperfusion injury, immune complexes, restenosis and parasitic diseases,
 CC to purify variant integrin polypeptide ligands and as bait proteins in
 CC two-hybrid or three-hybrid assays. This sequence represents a human
 CC integrin alpha subunit CD11b deletion variant A domain. Note: This
 CC variant sequence is not featured in the specification but has been
 CC derived from the wild-type protein shown in AAU76847

XX Sequence 177 AA;

Query Match 98.9%; Score 912; DB 5; Length 177;
 Best Local Similarity 98.3%; Pred. No. 2.6e-94;
 Matches 174; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 60
 DB 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 60
 QY 61 EFQNNPNRSLVKPTITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
 DB 61 EFQNNPNRSLVKPTITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
 QY 121 DPLGYEDVIPADREGVIRYVIGVDAPRSKRSQELNTIASKPPRDHVFQCNNEC 177
 DB 121 DPLGYEDVIPADREGVIRYVIGVDAPRSKRSQELNTIASKPPRDHVFQCNNEC 177

RESULT 2

AAV21991
 ID AAV21991 standard; protein; 187 AA.
 XX
 AC AAV21991;
 XX
 XX
 DT 13-SEP-1999 (first entry)
 XX Human complement factor MAC-1 vWF domain sequence.
 DE
 XX Factor B analogue; modified; complement activity; complement factor B;
 KW short consensus repeat domain; von Willebrand Factor domain; human; C2;
 KW CR3; autoimmune response; tissue damage; lupus erythematosus; therapy;
 KW rheumatoid arthritis; hemolytic anemia; myasthenia gravis; injury; MAC-1;
 KW myocardial infarction; acute shock lung syndrome; inflammation; vWF.
 XX
 OS Homo sapiens.
 XX
 XX US928892-A.
 FN
 XX
 PD 27-JUL-1999.
 XX
 XX 26-JUL-1996; 96US-00687706.
 PF
 XX
 PR 03-JAN-1994; 94US-00177109.
 XX
 XX (UNIW) UNIV WASHINGTON.
 PA
 XX Oglesby TJ, Hourcade DE;
 PI
 XX WPI; 1999-429498/36.
 DR
 XX Nucleic acids encoding complement protein homologues useful for
 PT modulating function of the complement system in the treatment of a
 PT variety of immune and autoimmune complex mediated syndromes.
 XX
 PS Disclosure; Fig 5A-B; S3pp; English.

XX The invention relates to a Factor B analogue that exhibits modified
 CC complement activity in vitro. The analogue is generated by substituting a
 CC short consensus repeat domain (SCR) or a von Willebrand Factor domain
 CC (vWF) of human factor B with a SCR or a vWF from a second protein such as
 CC human C2 or CR3. The analogues may be used to regulate the complement
 CC system involved in immune and autoimmune responses. Complement activity
 CC can account for substantial tissue damage in a wide variety of autoimmune
 CC /immune complex mediated syndromes such as lupus erythematosus,
 CC rheumatoid arthritis, hemolytic anemias and myasthenia gravis. Inhibition
 CC of the complement system using the analogues is likely to provide a means
 CC of therapeutic intervention in these cases. Inhibition of complement may
 CC also be favorable in cases that involve tissue damage caused by vascular
 CC injury such as myocardial infarction, cerebral vascular accidents or
 CC acute shock lung syndrome. In these cases the complement system may
 CC contribute to the destruction of partially damaged tissue as in
 CC reperfusion injury. In addition, the use of complement analogues with
 CC novel target specificities could reduce the activity of tissue damaging
 CC proteins at sites of inflammation. Complement inhibition is important in
 CC the prevention of xenograft rejection (the inhibition of complement by
 CC cell-associated and soluble inhibitors is useful in protecting the
 CC transplant from damage caused by activation of endogenous complement. The
 CC present sequence represents the vWF domain of human factor MAC-1

XX Sequence 187 AA;

Query Match 97.9%; Score 903; DB 2; Length 187;
 Best Local Similarity 99.4%; Pred. No. 2.9e-93;
 Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 60
 DB 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 60
 QY 61 EFQNNPNRSLVKPTITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
 DB 61 EFQNNPNRSLVKPTITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
 QY 121 DPLGYEDVIPADREGVIRYVIGVDAPRSKRSQELNTIASKPPRDHVFQCNNEC 176
 DB 121 DPLGYEDVIPADREGVIRYVIGVDAPRSKRSQELNTIASKPPRDHVFQCNNEC 176

RESULT 3

ADM99589
 ID ADM99589 standard; protein; 1152 AA.
 XX
 AC ADM99589;
 XX
 DT 17-JUN-2004 (first entry)
 XX Human integrin alphaM subunit precursor protein.
 DE
 XX integrin alpha subunit; beta; antipsoriatic; thrombolytic; anticoagulant;
 KW osteopathic; cytostatic; immunosuppressive; antiinflammatory;
 KW neuroprotective; antiskinning; immunotherapy; inflammatory;
 KW autoimmune disorder; thrombosis; cancer; osteoporosis;
 KW sickle cell anaemia; psoriasis; multiple sclerosis; human; precursor;
 KW alphasM.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Key
 FT Misc-difference 965 /note= "Encoded by CCC"
 FT
 XX
 XX WO2004007530-A2.
 FN
 XX
 PD 22-JAN-2004.
 XX
 PF 17-JUL-2003; 2003WO-US022301.
 XX
 XX 17-JUL-2002; 2002US-0396783P.
 PR

PR 17-JUL-2002; 2002US-0396790P.
PR 11-SEP-2002; 2002US-0410135P.
XX (BLOO-) CENT BLOOD RES INC.
XX Springer TA, Takagi J;
XX WPI; 2004-122877/12.
DR N-PSDB; ADM95588.
XX Novel modified integrin protein having extracellular domains of integrin
PT alpha and beta subunits or integrin alphaII and beta3 subunit, useful for
PT treating integrin mediated disorders.
XX
XX Disclosure; SEQ ID NO 4; 232pp; English.
XX
XX The invention relates to a novel isolated or recombinant modified
CC integrin protein having extracellular domains of integrin alpha and beta
CC subunits where one of the subunits has one or more mutations, an altered
CC surface feature or an amino acid substitution or internal deletion,
CC extracellular domains of the integrin beta subunit that comprise a
CC mutation that alters a non-cysteine residue to cysteine or extracellular
CC domains of integrin alpha and beta subunits. The polypeptide of the
CC invention demonstrates antipruritic, thrombolytic, anticoagulant,
CC osteopathic, cytostatic, immunosuppressive, antiinflammatory,
CC neuroprotective and anti-sickling activities and may be useful for
CC immunotherapy in order to prevent or treat an integrin-mediated disorder
CC such as an inflammatory disorder, an autoimmune disorder, thrombosis,
CC cancer, osteoporosis, sickle cell anaemia, psoriasis and multiple
CC sclerosis. The current sequence is that of the human integrin alpha
CC subunit precursor protein of the invention.
XX
XX
SQ Sequence 1152 AA;
Query Match 97.9%; Score 903; DB 8; Length 1152;
Best Local Similarity 99.4%; Pred. No. 3.7e-92;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTPK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDPRMKFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTPK 203
QY 61 EFQNNPNRSLVKPTQLLGRTHATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
DB 204 EFQNNPNRSLVKPTQLLGRTHATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 263
QY 121 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPRDRHVQCNFFE 176
DB 264 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPRDRHVQCNFFE 319
RESULT 4
ADP12435
ID ADP12435 standard; protein; 1152 AA.
XX
XX ADP12435;
DT 12-AUG-2004 (first entry)
XX
DE Protein encoded by mRNA of the invention #45.
XX
KW transplamt rejection; immune system; rheumatoid arthritis; lupus;
KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
XX
OS Homo sapiens.
XX
PN WO2004042346-A2.
XX
PD 21-MAY-2004.
XX
XX
PF 24-APR-2003; 2003WO-US012946.
XX
PR 24-APR-2002; 2002US-00131831.

PR 20-DEC-2002; 2002US-00325899.
XX (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX
XX Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
PI Rosenberg S;
XX WPI; 2004-400724/37.
XX
XX Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT rejection, in an individual, comprises detecting the expression level of
PT the genes.
XX
XX Claim 65; SEQ ID NO 2444; 1762pp; English.
XX
XX The present invention relates to diagnosing or monitoring transplant
CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
CC comprises detecting the expression level of one or more genes. The
CC methods, system and kits are useful in diagnosing or monitoring
CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
CC islet, lung, bone marrow or stem cell transplant rejection,
CC xenotransplant rejection or mechanical organ replacement rejection, in an
CC individual. The method is also useful in assessing the immune status of
CC an individual. The methods are also useful in diagnosing and monitoring
CC diseases that involve the immune system, e.g. rheumatoid arthritis,
CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
CC vital, bacterial or fungal infection. The present sequence represents a
CC protein that is encoded by the mRNA of the invention.
XX
XX
SQ Sequence 1152 AA;
Query Match 97.9%; Score 903; DB 8; Length 1152;
Best Local Similarity 99.4%; Pred. No. 3.7e-92;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTPK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDPRMKFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTPK 203
QY 61 EFQNNPNRSLVKPTQLLGRTHATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
DB 204 EFQNNPNRSLVKPTQLLGRTHATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 263
QY 121 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPRDRHVQCNFFE 176
DB 264 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPRDRHVQCNFFE 319
RESULT 5
AAR04136
ID AAR04136 standard; protein; 1153 AA.
XX
XX AAR04136;
XX
XX 09-SEP-2004 (revised)
DT 25-MAR-2003 (revised)
DT 07-SEP-1990 (first entry)
XX
DE Alpha subunit of Mac-1 leukocyte adhesion receptor.
XX
KW Mac-1 alpha subunit; Mac-1 alpha/beta heterodimer;
KW non-specific defence system; integrin gene superfamily.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 1..16
FT /label= signal_peptide
FT Modified-site 86..88
FT /label= putative N-glycosylation site
FT Modified-site 240..242
FT /label= putative N-glycosylation site

FT	Modified-site	391..393		QY	1	CPOEDSDIAFLIDSGSIIPHDFRMKEFVSTVMEQKSKTLFSLMOYSEEFRIHFTFK	60
FT	Modified-site	/label= putative N-glycosylation site					
FT	Modified-site	469..471		Db	144	CPOEDSDIAFLIDSGSIIPHDFRMKEFVSTVMEQKSKTLFSLMOYSEEFRIHFTFK	203
FT	Modified-site	/label= putative N-glycosylation site					
FT	Modified-site	693..695		QY	61	EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG	120
FT	Modified-site	697..699		Db	204	EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG	263
FT	Modified-site	/label= putative N-glycosylation site					
FT	Modified-site	735..737		QY	121	DPLGYEDVIEADREGVIRYVIGVDAFRSEKSRQELNTIASKPPRDHVFQNNFE	176
FT	Modified-site	/label= putative N-glycosylation site					
FT	Modified-site	802..804		Db	264	DPLGYEDVIEADREGVIRYVIGVDAFRSEKSRQELNTIASKPPRDHVFQNNFE	319
FT	Modified-site	/label= putative N-glycosylation site					
FT	Modified-site	881..883					
FT	Modified-site	/label= putative N-glycosylation site					
FT	Modified-site	901..903					
FT	Modified-site	/label= putative N-glycosylation site					
FT	Modified-site	912..914					
FT	Modified-site	/label= putative N-glycosylation site					
FT	Modified-site	941..943					
FT	Modified-site	/label= putative N-glycosylation site					
FT	Modified-site	947..949					
FT	Modified-site	/label= putative N-glycosylation site					
FT	Modified-site	979..981					
FT	Modified-site	/label= putative N-glycosylation site					
FT	Modified-site	994..996					
FT	Modified-site	/label= putative N-glycosylation site					
FT	Modified-site	1022..1024					
FT	Modified-site	/label= putative N-glycosylation site					
FT	Modified-site	1045..1047					
FT	Modified-site	/label= putative N-glycosylation site					
FT	Modified-site	1051..1053					
FT	Modified-site	/label= putative N-glycosylation site					
FT	Modified-site	1076..1078					
FT	Modified-site	/label= putative N-glycosylation site					
FT	Modified-site	1106..1134					
FT	Region	/label= putative_transmembrane_region					
XX	EP364690-A.						
PN	25-APR-1990.						
XX	17-AUG-1989;	89EP-00115159.					
XX	23-AUG-1988;	88US-00235353.					
PR	09-MAR-1989;	89US-00321239.					
XX	(DAND) DANA FARBER CANCER INST INC.						
PA	Springer TA, Corbi A;						
PI	WPI; 1990-125938/17.						
DR	N-PSDB; AAQ04043.						
XX	New pure Mac-1 alpha sub-unit and corresp. DNA - useful for treating inflammation and viral infections, and in diagnosis.						
PT	Disclosure; Page ?; 3pp; English.						
XX	Mac-1 alpha subunit is involved in the response to inflammation, i.e. recognition of and migration to sites of inflammation. It also attaches to cellular substrates as part of this function making it useful in visualising endothelial tissue. Mac-1 is a member of the Integrin Gene superfamily. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25 -MAR-2003 to correct PA field.)						
CC	Revised record issued on 09-SEP-2004 : Correction to feature table key and pages						
CC	Sequence 1153 AA;						
XX	Query Match	97.9%;	Score 903;	DB 2;	Length 1153;		
XX	Best Local Similarity	99.4%;	Pred. No. 3.7e-92;				
XX	Matches 175; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;		
SQ	Sequence 1153 AA;						
XX	Query Match	97.9%;	Score 903;	DB 2;	Length 1153;		
XX	Best Local Similarity	99.4%;	Pred. No. 3.7e-92;				
XX	Matches 175; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;		
SQ	Sequence 1153 AA;						
XX	Query Match	97.9%;	Score 903;	DB 2;	Length 1153;		
XX	Best Local Similarity	99.4%;	Pred. No. 3.7e-92;				
XX	Matches 175; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;		
SQ	Sequence 1153 AA;						
XX	Query Match	97.9%;	Score 903;	DB 2;	Length 1153;		
XX	Best Local Similarity	99.4%;	Pred. No. 3.7e-92;				
XX	Matches 175; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;		
SQ	Sequence 1153 AA;						
XX	Query Match	97.9%;	Score 903;	DB 2;	Length 1153;		
XX	Best Local Similarity	99.4%;	Pred. No. 3.7e-92;				
XX	Matches 175; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;		
SQ	Sequence 1153 AA;						
XX	Query Match	97.9%;	Score 903;	DB 2;	Length 1153;		
XX	Best Local Similarity	99.4%;	Pred. No. 3.7e-92;				
XX	Matches 175; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;		
SQ	Sequence 1153 AA;						
XX	Query Match	97.9%;	Score 903;	DB 2;	Length 1153;		
XX	Best Local Similarity	99.4%;	Pred. No. 3.7e-92;				
XX	Matches 175; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;		
SQ	Sequence 1153 AA;						
XX	Query Match	97.9%;	Score 903;	DB 2;	Length 1153;		
XX	Best Local Similarity	99.4%;	Pred. No. 3.7e-92;				
XX	Matches 175; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;		
SQ	Sequence 1153 AA;						
XX	Query Match	97.9%;	Score 903;	DB 2;	Length 1153;		
XX	Best Local Similarity	99.4%;	Pred. No. 3.7e-92;				
XX	Matches 175; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;		
SQ	Sequence 1153 AA;						
XX	Query Match	97.9%;	Score 903;	DB 2;	Length 1153;		
XX	Best Local Similarity	99.4%;	Pred. No. 3.7e-92;				
XX	Matches 175; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;		
SQ	Sequence 1153 AA;						
XX	Query Match	97.9%;	Score 903;	DB 2;	Length 1153;		
XX	Best Local Similarity	99.4%;	Pred. No. 3.7e-92;				
XX	Matches 175; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;		
SQ	Sequence 1153 AA;						
XX	Query Match	97.9%;	Score 903;	DB 2;	Length 1153;		
XX	Best Local Similarity	99.4%;	Pred. No. 3.7e-92;				
XX	Matches 175; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;		
SQ	Sequence 1153 AA;						
XX	Query Match	97.9%;	Score 903;	DB 2;	Length 1153;		
XX	Best Local Similarity	99.4%;	Pred. No. 3.7e-92;				
XX	Matches 175; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;		
SQ	Sequence 1153 AA;						
XX	Query Match	97.9%;	Score 903;	DB 2;	Length 1153;		
XX	Best Local Similarity	99.4%;	Pred. No. 3.7e-92;				
XX	Matches 175; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;		
SQ	Sequence 1153 AA;						
XX	Query Match	97.9%;	Score 903;	DB 2;	Length 1153;		
XX	Best Local Similarity	99.4%;	Pred. No. 3.7e-92;				
XX	Matches 175; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;		
SQ	Sequence 1153 AA;						
XX	Query Match	97.9%;	Score 903;	DB 2;	Length 1153;		
XX	Best Local Similarity	99.4%;	Pred. No. 3.7e-92;				
XX	Matches 175; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;		
SQ	Sequence 1153 AA;						
XX	Query Match	97.9%;	Score 903;	DB 2;	Length 1153;		
XX	Best Local Similarity	99.4%;	Pred. No. 3.7e-92;				
XX	Matches 175; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;		
SQ	Sequence 1153 AA;						
XX	Query Match	97.9%;	Score 903;	DB 2;	Length 1153;		
XX	Best Local Similarity	99.4%;	Pred. No. 3.7e-92;				
XX	Matches 175; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;		
SQ	Sequence 1153 AA;						
XX	Query Match	97.9%;	Score 903;	DB 2;	Length 1153;		
XX	Best Local Similarity	99.4%;	Pred. No. 3.7e-92;				
XX	Matches 175; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;		
SQ	Sequence 1153 AA;						
XX	Query Match	97.9%;	Score 903;	DB 2;	Length 1153;		
XX	Best Local Similarity	99.4%;	Pred. No. 3.7e-92;				
XX	Matches 175; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;		
SQ	Sequence 1153 AA;						
XX	Query Match	97.9%;	Score 903;	DB 2;	Length 1153;		
XX	Best Local Similarity	99.4%;	Pred. No. 3.7e-92;				
XX	Matches 175; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;		
SQ	Sequence 1153 AA;						
XX	Query Match	97.9%;	Score 903;	DB 2;	Length 1153;		
XX	Best Local Similarity	99.4%;	Pred. No. 3.7e-92;				
XX	Matches 175; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;		
SQ	Sequence 1153 AA;						
XX	Query Match	97.9%;	Score 903;	DB 2;	Length 1153;		
XX	Best Local Similarity	99.4%;	Pred. No. 3.7e-92;				
XX	Matches 175; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;		
SQ	Sequence 1153 AA;						
XX	Query Match	97.9%;	Score 903;	DB 2;	Length 1153;		
XX	Best Local Similarity	99.4%;	Pred. No. 3.7e-92;				
XX	Matches 175; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;		
SQ	Sequence 1153 AA;						
XX	Query Match	97.9%;	Score 903;	DB 2;	Length 1153;		
XX	Best Local Similarity	99.4%;	Pred. No. 3.7e-92;				
XX	Matches 175; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;		
SQ	Sequence 1153 AA;						
XX	Query Match	97.9%;	Score 903;	DB 2;	Length 1153;		
XX	Best Local Similarity	99.4%;	Pred. No. 3.7e-92;				
XX	Matches 175; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;		
SQ	Sequence 1153 AA;						
XX	Query Match	97.9%;	Score 903;	DB 2;	Length 1153;		
XX	Best Local Similarity	99.4%;	Pred. No. 3.7e-92;				
XX	Matches 175; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;		
SQ	Sequence 1153 AA;						
XX	Query Match	97.9%;	Score 903;	DB 2;	Length 1153;		
XX	Best Local Similarity	99.4%;	Pred. No. 3.7e-92;				
XX	Matches 175; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;		
SQ	Sequence 1153 AA;						
XX	Query Match	97.9%;	Score 903;	DB 2;	Length 1153;		
XX	Best Local Similarity	99.4%;	Pred. No. 3.7e-92;				
XX	Matches 175; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;		
SQ	Sequence 1153 AA;						
XX	Query Match	97.9%;	Score 903;	DB 2;	Length 1153;		
XX	Best Local Similarity	99.4%;	Pred. No. 3.7e-92;				
XX	Matches 175; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;		
SQ	Sequence 1153 AA;						
XX	Query Match	97.9%;	Score 903;	DB 2;	Length 1153;		
XX	Best Local Similarity	99.4%;	Pred. No. 3.7e-92;				
XX	Matches 175; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;		
SQ	Sequence 1153 AA;						
XX	Query Match	97.9%;	Score 903;	DB 2;	Length 1153;		
XX	Best Local Similarity	99.4%;	Pred. No. 3.7e-92;				
XX	Matches 175; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;		
SQ	Sequence 1153 AA;						
XX	Query Match	97.9%;	Score 903;	DB 2;	Length 1153;		
XX	Best Local Similarity	99.4%;	Pred. No. 3.7e-92;				
XX	Matches 175; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;		
SQ	Sequence 1153 AA;						
XX	Query Match	97.9%;	Score 903;	DB 2;	Length 1153;		
XX	Best Local Similarity	99.4%;	Pred. No. 3.7e-92;				
XX	Matches 175; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;		
SQ	Sequence 1153 AA;						
XX	Query Match	97.9%;	Score 903;	DB 2;	Length 1153;		
XX	Best Local Similarity	99.4%;	Pred. No. 3.7e-92;				
XX	Matches 175; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;		
SQ	Sequence 1153 AA;						
XX	Query Match	97.9%;	Score 903;	DB 2;	Length 1153;		
XX	Best Local Similarity	99.4%;	Pred. No. 3.7e-92;				
XX	Matches 175; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;		
SQ	Sequence 1153 AA;						
XX	Query Match	97.9%;	Score 903;	DB 2;	Length 1153;		
XX	Best Local Similarity	99.4%;	Pred. No. 3.7e-92;				
XX	Matches 175; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;		
SQ	Sequence 1153 AA;						
XX	Query Match	97.9%;	Score 903;	DB 2;	Length 1153;		
XX	Best Local Similarity	99.4%;	Pred. No. 3.7e-92;				
XX	Matches 175; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;		
SQ	Sequence 1153 AA;						
XX	Query Match	97.9%;	Score 903;	DB 2;	Length 1153;		
XX	Best Local Similarity	99.4%;	Pred. No. 3.7e-92;				
XX	Matches 175; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;		
SQ	Sequence 1153 AA;						
XX	Query Match	97.9%;	Score 903;	DB 2;	Length 1153;		
XX	Best Local Similarity	99.4%;	Pred. No. 3.7e-92;				
XX	Matches 175;						

Db 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSEFRHFTFK 203
QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
Db 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQCNPE 176
Db 264 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQCNPE 319

RESULT 7
AAB07360
ID AAB07360 standard; protein; 1153 AA.
XX
AC AAB07360;
DT 17-JAN-2001 (first entry)
XX
DE Human CD11b protein sequence.
XX
KW Human; macrophage infiltration inhibition; alpha d integrin;
KW leukocyte integrin; Leu-CAM; leukointegrin; immune response;
KW inflammation; leukocyte adhesion deficiency; LAD; Type I diabetes;
KW atherosclerosis; multiple sclerosis; asthma; psoriasis; beta2 integrin;
KW lung inflammation; acute respiratory distress syndrome; Crohn's disease;
KW rheumatoid arthritis; central nervous system injury; CD11b.
XX
OS Homo sapiens.
XX
XX
PN WO200029446-A1.
XX
XX 25-MAY-2000.
XX
PF 16-NOV-1999; 99WO-US027139.
XX
XX 16-NOV-1998; 98US-00193043.
PR 08-JUL-1999; 99US-00350259.
XX
XX (ICOS-) ICOS CORP.
XX
XX Gallatin MW, Van Der Vieren M;
PI WPI; 2000-387751/33.
XX
DR WPI; 2000-387751/33.
XX
PT Use of novel anti-alpha integrin d monoclonal antibodies to inhibit
PT macrophage infiltration and reduce inflammation at central nervous system
PT injury sites.
XX
PS Example 5; Fig 1; 270pp; English.
XX
CC Integrins are a class of membrane-associated molecules that participate
CC in cellular adhesion. Integrins are made up of an alpha subunit and a
CC beta subunit. One class of human integrins are restricted to expression
CC in white blood cells and have a common beta2 subunit: the leukocyte
CC integrins, Leu-CAMs, leukointegrins or beta2 integrins. Beta2 integrins
CC have an important role in immune and inflammatory responses. The present
CC protein sequence is the human integrin alpha subunit CD11b. This sequence
CC was used in an alignment to identify a novel beta2 integrin alpha
CC subunit: alpha_d (AAK60014 and AAB07359). The present sequence has
CC approximately 60% identity to the protein sequence of alpha_d. The
CC Alpha_d gene and protein may be useful in therapy for diseases linked to
CC aberrant alpha_d function e.g. Type I diabetes, atherosclerosis, multiple
CC sclerosis, asthma, psoriasis, lung inflammation, acute respiratory
CC distress syndrome, rheumatoid arthritis and leukocyte adhesion deficiency
CC (LAD). In addition, anti-alpha_d monoclonal antibodies may be used in the
CC inhibition of macrophage infiltration at the site of a central nervous
CC system injury. The monoclonal antibodies can also be used to detect and
CC diagnose Crohn's disease
XX
SQ Sequence 1153 AA;

Query Match 97.9%; Score 903; DB 3; Length 1153;
Best Local Similarity 99.4%; Pred. No. 3.7e-92;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSEFRHFTFK 60
Db 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSEFRHFTFK 203
QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
Db 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQCNPE 176
Db 264 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQCNPE 319

RESULT 8
AAB080252
ID AAB080252 standard; protein; 1153 AA.
XX
AC AAB080252;
DT 15-JUL-2002 (first entry)
XX
DE Human integrin 1 alpha-M subunit protein.
XX
KW Integrin; antiinflammatory; immunosuppression; nephritis; dermatitis;
KW inflammatory disease; autoimmune disorder; Crohn's disease;
KW human immunodeficiency virus; HIV; myocardial infarction;
KW Sjorgen's syndrome; rheumatoid arthritis.
XX
XX Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 499..500 /note= "Encoded by GGG CAG AGG"
FT
XX
PN WO200218583-A2.
XX
PD 07-MAR-2002.
XX
PF 31-AUG-2001; 2001WO-US027227.
XX
PR 01-SEP-2000; 2000US-0229700P.
PA (BLOO-) CENT BLOOD RES INC.
XX
XX Springer TA, Shimoaka M, Lu C;
PI
XX
DR WPI; 2002-382964/41.
DR N-PSDB; ABK50046.
XX
XX Modified integrin-I or integrin I-like domain polypeptide useful as an
PT immunogen to produce antibodies specific to polypeptide, comprises a
PT disulfide bond such that polypeptide is stabilized in a desired
PT conformation.
XX
PS Disclosure; Page 109-112; 112pp; English.
XX
CC This invention relates to a modified integrin-I or integrin I-like domain
CC polypeptide comprising at least one disulfide bond so that the domain is
CC stabilised in a desired conformation. The polypeptide of the invention
CC may have antiinflammatory or immunosuppressive activities. The
CC polypeptides of the invention have an open conformation and are useful as
CC immunogens to produce antibodies that selectively bind to integrin I-
CC domain; and for identifying a modulator of integrin activity, or of
CC interaction of an integrin and a cognate ligand. The polypeptide of the
CC invention, or antibodies (preferably anti-LFA-1 antibody) is useful for
CC treating or preventing an integrin mediated disorder which is an
CC inflammatory or autoimmune disorder in a subject and for inhibiting the
CC binding of an integrin to a cognate ligand such as Crohn's disease,
CC nephritis; human immunodeficiency virus (HIV), myocardial infarction,

CC Sjorgen's syndrome, rheumatoid arthritis, dermatitis. A therapeutic
CC composition comprising the peptide of the invention is useful for
CC treating an integrin mediated disorder in a subject. The polypeptides
CC and/or active or antigenic fragments are useful as reagents for diagnosis
CC of integrin-mediated disorders. The present sequence represents the human
CC integrin-1 alpha-M protein subunit used to generate the mutant
CC polypeptides of the invention
XX
SQ Sequence 1153 AA;

Query Match 97.9%; Score 903; DB 5; Length 1153;
Best Local Similarity 99.4%; Pred. No. 3.7e-92;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTSLFSLMOYSEEFRIHFTFK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTSLFSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQNNPE 176
DB 264 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQNNPE 319

RESULT 9

ID ABG61469

XX ABG61469 standard; protein; 1153 AA.

AC ABG61469;

DT 27-AUG-2002 (first entry)

XX Human Beta2 integrin alphaCD11b subunit.

XX Beta2 integrin; alphaD subunit; CD11c subunit; LAD;
KW leukocyte adhesion deficiency; inflammatory response; diabetes;
KW multiple sclerosis; arthritis; graft atherosclerosis; neuroprotective;
KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW immune complex alveolitis; leukaemia; ICAM-R; VCAM-1; anti-inflammatory;
KW intracellular cell adhesion molecule; vascular cell adhesion molecule;
KW locomotor recovery; locomotor damage; locomotor impairment;
KW autonomic dysfunction; sensory dysfunction; spinal cord injury.

XX Homo sapiens.

XX WO200230980-A2.

XX 18-APR-2002.

PF 15-OCT-2001; 2001WO-US032059.

XX 13-OCT-2000; 2000US-00688307.

XX (ICOS-) ICOS CORP.

XX Gallatin WM, Van Der Vieren M;

XX WPI; 2002-463260/49.

XX Use of an anti-alpha-d monoclonal antibodies for promoting locomotor
PT recovery, inhibiting locomotor damage, limiting locomotor impairment, or
PT limiting autonomic and sensory dysfunction following spinal cord injury.

XX Example 5; Page 191-194; 270pp; English.

XX The invention relates to promoting locomotor recovery, inhibiting
CC locomotor damage, limiting locomotor impairment, or limiting autonomic
CC and sensory dysfunction following spinal cord injury by administering an
CC anti-alpha d (Beta2 integrin alpha2 subunit) monoclonal antibody to a
CC spinal cord injury victim. The method also involves the use of a ligand

CC selected from ICAM-R or VCAM-1 (intracellular cell adhesion molecule,
CC vascular cell adhesion molecule). The method is useful for promoting
CC locomotor recovery, inhibiting locomotor damage, limiting locomotor
CC impairment, or limiting autonomic and sensory dysfunction following
CC spinal cord injury. In particular, the spinal cord injury comprises
CC compression of the spinal cord. The antibodies are also useful for
CC reducing inflammation at the site of a central nervous system injury. The
CC specification also details the identification of Beta2 integrin alphaD
CC cDNAs and proteins, for use in raising the antibodies. Beta2 integrins
CC are implicated in diseases such as LAD (leukocyte adhesion deficiency,
CC inflammatory response, diabetes, multiple sclerosis, arthritis, graft
CC atherosclerosis, inflammatory bowel disease, Crohn's disease, ulcerative
CC colitis, immune complex alveolitis and leukaemia. The present sequence is
CC a Beta2 integrin alpha subunit sequence included for comparison with the
CC Beta2 integrin alphaD protein sequences
XX
SQ Sequence 1153 AA;

Query Match 97.9%; Score 903; DB 5; Length 1153;
Best Local Similarity 99.4%; Pred. No. 3.7e-92;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTSLFSLMOYSEEFRIHFTFK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTSLFSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQNNPE 176
DB 264 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQNNPE 319

RESULT 10

AAO14428

ID AAO14428 standard; protein; 1153 AA.

XX AAO14428;

AC AAO14428;

DT 03-MAY-2002 (first entry)

XX Integrin Mac-1 alpha subunit.

XX Mac-1; integrin alpha subunit; variant integrin inserted domain protein;
KW open conformation; integrin related inflammatory disorder;
KW integrin related immunological disorder; rheumatoid arthritis; ischaemia;
KW reperfusion; hypovolemic shock; infarction; cerebral shock;
KW viral infection; cancer; gene therapy; vaccine;
KW bioactive agent screening.

XX Unidentified.

XX WO200204521-A2.

XX 17-JAN-2002.

PF 09-JUL-2001; 2001WO-US021805.

XX 07-JUL-2000; 2000US-0216600P.

XX (CALY) CALIFORNIA INST OF TECHNOLOGY.

PA (BLOO-) CENT BLOOD RES.

XX Springer T;

XX WPI; 2002-148167/19.

XX New integrin I domain protein having alteration in at least 2
PT noncontiguous regions and exits in an open conformation, useful for
PT treating, preventing or suppressing inflammatory or immunological
PT disorders.

```
XX PS Example 1; Fig 1F; 90pp; English.
XX CC The invention comprises structurally biased variant integrin inserted (I)
CC CC domain proteins, wherein the alterations to the protein occur in at least
CC CC two noncontinuous regions. Specifically the variant integrin I domain
CC CC proteins are structurally biased to exist in the open conformation,
CC CC thereby altering the binding ability of the protein. The invention also
CC CC comprises nucleic acids encoding the variant integrin I domain proteins.
CC CC The integrin I domain proteins and nucleic acids are useful for treating,
CC CC preventing or suppressing integrin related inflammatory and immunological
CC CC disorders (e.g. rheumatoid arthritis). The variant integrin I domain
CC CC proteins and nucleic acids can also be used for treating: ischaemia/
CC CC reperfusion (e.g. hypovolemic shock); infarction; cerebral shock; viral
CC CC infection; and cancer. The variant integrin I domain nucleic acids and
CC CC proteins may be used in gene therapy, as vaccines and to screen for
CC CC bioactive agents. The present amino acid sequence represents the Mac-1
CC CC alpha subunit of integrin
XX SQ Sequence 1153 AA;

Query Match          97.9%; Score 903; DB 5; Length 1153;
Best Local Similarity 99.4%; Pred No. 3.7e-92;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMQYSEEFRIHFTFK 60
DB 144 CPQEDSDIAFLIDSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMQYSEEFRIHFTFK 203

QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 263

QY 121 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQCNFFE 176
DB 264 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQCNFFE 319

RESULT 11
ADD25615
ID ADD25615 standard; protein; 1153 AA.
AC ADD25615;
XX 15-JAN-2004 (first entry)
DE Binding domain-immunoglobulin fusion protein-associated protein #85.
XX Binding domain; immunoglobulin; fusion protein; cytostatic;
XX antiarthritic; immunosuppressive; antidiabetic; antithyroid;
XX neuroprotective; hinge region; immunoglobulin heavy chain;
XX CH2 constant region; CH3 constant region; IG1;
XX antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
XX malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
XX rheumatoid arthritis; myasthenia gravis; Grave's disease;
XX type 1 diabetes mellitus; multiple sclerosis; autoimmune disease.
XX OS Unidentified.
XX US2003118592-A1.
XX 26-JUN-2003.
XX 25-JUL-2002; 2002US-00207655.
XX 17-JAN-2001; 2001US-0367358P.
XX 17-JAN-2002; 2002US-00053530.
XX 03-JUN-2002; 2002US-0385691P.
XX (GENE-) GENE-CRAFT INC.
XX Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
XX
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DR WPI; 2003-801317/75.
XX New binding domain-immunoglobulin fusion protein, useful for treating a
PT subject having or suspected of having a malignant condition or a B-cell
PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.
XX Disclosure; SEQ ID NO 176; 157pp; English.
XX The invention relates to a binding domain-immunoglobulin fusion protein
CC comprising a binding domain polypeptide that is fused to an
CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain
CC CH2 constant region polypeptide that is fused to the hinge region
CC polypeptide, and an immunoglobulin heavy chain CH3 constant region
CC polypeptide that is fused to the CH2 constant region polypeptide. The
CC hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin
CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge
CC region polypeptide; derived from (a) having 3 or more cysteine residues;
CC where the mutated human IgG1 immunoglobulin hinge region polypeptide
CC contains 2 cysteine residues, where the first cysteine is not mutated; a
CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from
CC (a) having 3 or more cysteine residues, where the mutated human IgG1
CC immunoglobulin hinge region polypeptide contains no more than one
CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region
CC polypeptide, derived from (a) having 3 or more cysteine residues; where
CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains
CC no cysteine residues. The binding domain-immunoglobulin fusion protein is
CC capable of at least one immunological activity comprising antibody
CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The
CC binding domain polypeptide is capable of specifically binding to an
CC antigen. Also included are an isolated polynucleotide encoding the
CC binding domain-immunoglobulin fusion protein, a recombinant expression
CC construct comprising the polynucleotide (operably linked to a promoter),
CC a host cell transformed or transfected with a recombinant expression
CC construct, producing the binding domain-immunoglobulin fusion protein, a
CC pharmaceutical composition comprising the binding domain-immunoglobulin
CC fusion protein or polynucleotide and a carrier, and treating a subject
CC having or suspected of having a malignant condition or a B-cell disorder.
CC The binding domain-immunoglobulin fusion protein is useful for treating a
CC subject having or suspected of having a malignant condition or a B-cell
CC disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,
CC myasthenia gravis, Grave's disease, type 1 diabetes mellitus, multiple
CC sclerosis or autoimmune disease. The present sequence is a binding domain
CC -immunoglobulin fusion protein-associated protein sequence. Note: The
CC sequence data for this patent formed part of the printed specification
CC and is also available in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030118592. The authors have not
CC identified the sequences in the printed specification by their SEQ ID
CC number therefore none of the sequences can be explicitly identified.
XX SQ Sequence 1153 AA;

Query Match          97.9%; Score 903; DB 7; Length 1153;
Best Local Similarity 99.4%; Pred No. 3.7e-92;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMQYSEEFRIHFTFK 60
DB 144 CPQEDSDIAFLIDSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMQYSEEFRIHFTFK 203

QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 263

QY 121 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQCNFFE 176
DB 264 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQCNFFE 319

RESULT 12
AAU76865
ID AAU76865 standard; protein; 177 AA.
XX AAU76865;
AC AAU76865;
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XX DT 21-MAY-2002 (first entry)
 XX DE Human integrin alpha subunit CD11b deletion variant A domain #1.
 XX KW Human; integrin alpha subunit; A domain; CD11b; integrin beta subunit;
 KW A-like domain; inflammatory disorder; skeletal muscle injury; restenosis;
 KW ischaemia-reperfusion injury; immune complex; parasitic disease; mutant;
 KW antiinflammatory; vasotropic; antiparasitic; vulnerary; gene therapy;
 KW mtein.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 XX FT Misc-difference 170
 XX FT Misc-difference 177 /note= "Wild-type Phe substituted by Cys"
 XX FT Misc-difference 177 /note= "Wild-type Ala substituted by Cys"
 XX PN WO200209737-A1.
 XX PD 07-FEB-2002.
 XX PF 31-JUL-2001; 2001WO-US023957.
 XX PR 31-JUL-2000; 2000US-0221950P.
 XX PR 11-JAN-2001; 2001US-00758493.
 XX PR 13-MAR-2001; 2001US-00805354.
 XX PA (GEO) GEN HOSPITAL CORP.
 XX PI Arnaout AM, Li R, Xiong J;
 XX DR WPI; 2002-188687/24.
 XX PT Novel high affinity integrin polypeptide useful for treating restenosis
 PT and parasitic diseases, comprises all or part of variant integrin alpha
 PT subunit A domain or variant integrin beta subunit A-like domain.
 XX PS Claim 19; Page; 55pp; English.
 XX CC The invention relates to a high affinity integrin polypeptide comprising
 CC all or part of a variant integrin alpha subunit A domain or a variant
 CC integrin beta subunit A-like domain. The polypeptide, preferably the
 CC CD11b alpha subunit A domain, where I at residue 332 has been replaced by
 CC G or A, F at residue 313 and A at residue 320 have been replaced by C, or
 CC V at residue 315 and A at residue 320 have been replaced by C, is useful
 CC for determining if a test compound is a candidate compound for binding to
 CC CD11b or for treating an inflammatory disorder, by contacting a test
 CC compound with the polypeptide and determining if the test compound binds
 CC to the polypeptide. The integrin subunits are useful for reducing
 CC skeletal muscle injury, for treating disorders caused by ischaemia-
 CC reperfusion injury, immune complexes, restenosis and parasitic diseases,
 CC to purify variant integrin polypeptide ligands and as bait proteins in
 CC two-hybrid or three-hybrid assays. This sequence represents a human
 CC integrin alpha subunit CD11b deletion variant A domain. Note: This
 CC variant sequence is not featured in the specification but has been
 CC derived from the wild-type protein shown in AAU76847
 XX SQ Sequence 177 AA;
 Query Match 97.0%; Score 894; DB 5; Length 177;
 Best Local Similarity 97.2%; Pred. No. 2.8e-92;
 Matches 172; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKGFVSTVMEQLKSKTFLSLMYSEFRIHFTFK 60
 DB 1 CPQEDSDIAFLIDGSGSIIPHDPRMKGFVSTVMEQLKSKTFLSLMYSEFRIHFTFK 60
 QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNTNGARKNAFKLLVLTGDKFG 120
 DB 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNTNGARKNAFKLLVLTGDKFG 120

QY 121 DPLGYEDVPEADREGVIRYVIGVDAPRSKSRQELNTIASKPRDRHVFCQNNPEC 177
 DB 121 DPLGYEDVPEADREGVIRYVIGVDAPRSKSRQELNTIASKPRDRHVFCQNNPEC 177
 RESULT 13
 ID AAU76856
 XX AAU76856 standard; protein; 191 AA.
 AC AAU76856;
 XX 21-MAY-2002 (first entry)
 XX Human integrin alpha subunit CD11b variant A domain.
 XX KW Human; integrin alpha subunit; A domain; CD11b; integrin beta subunit;
 KW A-like domain; inflammatory disorder; skeletal muscle injury; restenosis;
 KW ischaemia-reperfusion injury; immune complex; parasitic disease; mutant;
 KW antiinflammatory; vasotropic; antiparasitic; vulnerary; gene therapy;
 KW mtein.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 XX FT Misc-difference 189
 XX FT /label= Gly, Ala
 XX FT /note= "Wild-type Ile substituted by Gly or Ala"
 XX PN WO200209737-A1.
 XX PD 07-FEB-2002.
 XX PF 31-JUL-2001; 2001WO-US023957.
 XX PR 31-JUL-2000; 2000US-0221950P.
 XX PR 11-JAN-2001; 2001US-00758493.
 XX PR 13-MAR-2001; 2001US-00805354.
 XX PA (GEO) GEN HOSPITAL CORP.
 XX PI Arnaout AM, Li R, Xiong J;
 XX DR WPI; 2002-188687/24.
 XX PT Novel high affinity integrin polypeptide useful for treating restenosis
 PT and parasitic diseases, comprises all or part of variant integrin alpha
 PT subunit A domain or variant integrin beta subunit A-like domain.
 XX PS Claim 2; Page; 55pp; English.
 XX CC The invention relates to a high affinity integrin polypeptide comprising
 CC all or part of a variant integrin alpha subunit A domain or a variant
 CC integrin beta subunit A-like domain. The polypeptide, preferably the
 CC CD11b alpha subunit A domain, where I at residue 332 has been replaced by
 CC G or A, F at residue 313 and A at residue 320 have been replaced by C, or
 CC V at residue 315 and A at residue 320 have been replaced by C, is useful
 CC for determining if a test compound is a candidate compound for binding to
 CC CD11b or for treating an inflammatory disorder, by contacting a test
 CC compound with the polypeptide and determining if the test compound binds
 CC to the polypeptide. The integrin subunits are useful for reducing
 CC skeletal muscle injury, for treating disorders caused by ischaemia-
 CC reperfusion injury, immune complexes, restenosis and parasitic diseases,
 CC to purify variant integrin polypeptide ligands and as bait proteins in
 CC two-hybrid or three-hybrid assays. This sequence represents a human
 CC integrin alpha subunit CD11b variant A domain. Note: This variant
 CC sequence is not featured in the specification but has been derived from
 CC the wild-type protein shown in AAU76847
 XX SQ Sequence 191 AA;
 Query Match 96.9%; Score 893; DB 5; Length 191;

Best Local Similarity 97.7%; Pred. No. 4e-92; Mismatches 2; Indels 0; Gaps 0;
Matches 172; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTFK 60
DB 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTFK 60
QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNTNGARKNAFKLLVLTGDKFG 120
DB 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNTNGARKNAFKLLVLTGDKFG 120
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQNNFE 176
DB 121 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQNNFE 176

RESULT 14
AAU76847
ID AAU76847 standard; protein; 191 AA.
XX
AC AAU76847;
DT 21-MAY-2002 (first entry)
DE Human integrin alpha subunit CD11b A domain.
XX
KW Human; integrin alpha subunit; A domain; CD11b; integrin beta subunit;
KW A-like domain; inflammatory disorder; skeletal muscle injury; restenosis;
KW ischaemia-reperfusion injury; immune complex; parasitic disease;
KW antinflammatory; vasotropic; antiparasitic; vulnerary; gene therapy.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 1..188
FT /note= "This region is specifically claimed"
XX
PN WO200209737-A1.
XX
PD 07-FEB-2002.
XX
PF 31-JUL-2001; 2001WO-US023957.
XX
PR 31-JUL-2000; 2000US-0221950P.
PR 11-JAN-2001; 2001US-00758493.
PR 13-MAR-2001; 2001US-00805354.
XX
PA (GEO) GEN HOSPITAL CORP.
XX
PI Arnaout AM, Li R, Xiong J;
XX
DR WPI; 2002-188687/24.
XX
PT Novel high affinity integrin polypeptide useful for treating restenosis
PT and parasitic diseases, comprises all or part of variant integrin alpha
PT subunit A domain or variant integrin beta subunit A-like domain.
XX
PS Example 2; Fig 5; 55pp; English.
XX
CC The invention relates to a high affinity integrin polypeptide comprising
CC all or part of a variant integrin alpha subunit A domain or a variant
CC integrin beta subunit A-like domain. The polypeptide, preferably the
CC CD11b alpha subunit A domain, where I at residue 332 has been replaced by
CC G or A, F at residue 313 and A at residue 320 have been replaced by C, or
CC V at residue 315 and A at residue 320 have been replaced by C, is useful
CC for determining if a test compound is a candidate compound for binding to
CC CD11b or for treating an inflammatory disorder, by contacting a test
CC compound with the polypeptide and determining if the test compound binds
CC to the polypeptide. The integrin subunits are useful for reducing
CC skeletal muscle injury, for treating disorders caused by ischaemia-
CC reperfusion injury, immune complexes, restenosis and parasitic diseases,
CC to purify variant integrin polypeptide ligands and as bait proteins in
CC two-hybrid or three-hybrid assays. This sequence represents the human

CC integrin alpha subunit CD11b A domain
XX Sequence 191 AA;
Query Match 96.9%; Score 893; DB 5; Length 191;
Best Local Similarity 97.7%; Pred. No. 4e-92; Mismatches 2; Indels 0; Gaps 0;
Matches 172; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTFK 60
DB 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTFK 60
QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNTNGARKNAFKLLVLTGDKFG 120
DB 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNTNGARKNAFKLLVLTGDKFG 120
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQNNFE 176
DB 121 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQNNFE 176

RESULT 15
AAB66766
ID AAB66766 standard; protein; 216 AA.
XX
AC AAB66766;
DT 10-APR-2001 (first entry)
DE Amino acids 149-353 of human CR-3 alpha chain and His tag.
XX
KW EST; expressed sequence tag; inclusion body; binding partner;
KW immunoglobulins.
OS Homo sapiens.
OS Synthetic.
XX
PN WO200102588-A2.
XX
PD 11-JAN-2001.
XX
PF 30-JUN-2000; 2000WO-EP006137.
XX
PR 02-JUL-1999; 99EP-00112815.
XX
PA (MORP-) MORPHOSYS AG.
XX
PI Frisch C, Kretzschmar T, Hoess A, Von Rueden T;
XX
DR WPI; 2001-147085/15.
XX
PT Generating specific binding partners to (poly)peptides encoded by genomic
PT DNA fragments, involves forming inclusion bodies by expressing the
PT (poly)peptide as part of fusion proteins.
XX
PS Disclosure; Page 18; 45pp; English.
XX
CC The present invention relates to generating a specific binding partner to
CC a peptide, encoded by a genomic DNA fragment or an expressed sequence tag
CC (EST). A nucleic acid molecule encoding a fusion protein is expressed in
CC a host cell to allow the formation of inclusion bodies comprising the
CC fusion protein, the inclusion bodies are isolated and a specific binding
CC partner is generated. The specific binding partners generated are useful
CC for identifying and characterizing naturally occurring proteins e.g. as
CC immunoglobulins or fragments in immunoassays
XX
SQ Sequence 216 AA;
Query Match 94.5%; Score 871; DB 4; Length 216;
Best Local Similarity 99.4%; Pred. No. 1.4e-89;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 SDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTFKFQNN 65

Db	12	SDIAFLIDGSGSII PHDFRMEKFVSTVWEQLKSKTFLSLMOYSEEFRIHFTFEFQNN	71
Qy	66	PNPRSLVKPTITQLGRTHATGIRKVVREL FNTNGARKNAFKILVITDGEKFGDPLGY	125
Db	72	PNPRSLVKPTITQLGRTHATGIRKVVREL FNTNGARKNAFKILVITDGEKFGDPLGY	131
Qy	126	EDVIPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQNNFE	176
Db	132	EDVIPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQNNFE	182

Search completed: January 13, 2005, 15:12:33
Job time : 34.0928 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 13, 2005, 15:13:36 ; Search time 29.2475 Seconds
(without alignments)
2186.449 Million cell updates/sec

Title: RWHULB-C_COPY_144_320

Perfect score: 922

Sequence: 1 CPQEDSDIAFLIDGSGSIIP.....NTIASKPPRDHVFQCNNEC 177

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PT_NEW_PUB.pcp:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pcp:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pcp:*
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6: /cgn2_6/ptodata/2/pubpaa/PTUS_PUBCOMB.pcp:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pcp:*
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10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pcp:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pcp:*
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pcp:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pcp:*
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18: /cgn2_6/ptodata/2/pubpaa/US10F_PUBCOMB.pcp:*
19: /cgn2_6/ptodata/2/pubpaa/US10G_PUBCOMB.pcp:*
20: /cgn2_6/ptodata/2/pubpaa/US10H_PUBCOMB.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	903	97.9	191	10	US-09-805-354-1
2	903	97.9	191	11	US-09-758-493-1
3	903	97.9	191	14	US-10-144-259-1
4	903	97.9	1152	9	US-09-945-265-4
5	903	97.9	1153	9	US-09-350-259-3
6	903	97.9	1153	10	US-09-902-481A-1
7	903	97.9	1153	10	US-09-891-943-3
8	903	97.9	1153	14	US-10-144-259-30
9	903	97.9	1153	14	US-10-207-655-176
10	894	97.0	1137	10	US-09-902-481A-6
11	889	96.4	1137	10	US-09-902-481A-5
12	879	95.3	1137	10	US-09-902-481A-4
13	877	95.1	184	15	US-10-346-863-17

14	877	95.1	187	15	US-10-346-863-37	Sequence 37, Appl
15	877	95.1	187	16	US-10-615-515-9	Sequence 9, Appl
16	871	94.5	190	15	US-10-346-863-42	Sequence 42, Appl
17	871	94.5	190	15	US-10-346-863-48	Sequence 48, Appl
18	871	94.5	216	10	US-09-795-872-5	Sequence 5, Appl
19	871	94.5	216	16	US-10-662-824-5	Sequence 5, Appl
20	871	94.5	1137	10	US-09-902-481A-3	Sequence 3, Appl
21	683	74.1	199	14	US-10-066-551-11	Sequence 11, Appl
22	683	74.1	199	17	US-10-665-990A-11	Sequence 11, Appl
23	559	60.6	413	9	US-09-350-259-101	Sequence 101, App
24	559	60.6	413	10	US-09-891-943-101	Sequence 101, App
25	550	59.7	1151	9	US-09-350-259-37	Sequence 37, Appl
26	550	59.7	1151	10	US-09-891-943-37	Sequence 37, Appl
27	550	59.7	1161	9	US-09-350-259-55	Sequence 55, Appl
28	550	59.7	1161	10	US-09-891-943-55	Sequence 55, Appl
29	545	59.1	191	10	US-09-805-354-3	Sequence 3, Appl
30	545	59.1	191	11	US-09-758-493-3	Sequence 3, Appl
31	545	59.1	191	14	US-10-144-259-3	Sequence 3, Appl
32	545	59.1	1161	9	US-09-350-259-2	Sequence 2, Appl
33	545	59.1	1161	9	US-09-350-259-99	Sequence 99, Appl
34	545	59.1	1161	10	US-09-891-943-2	Sequence 2, Appl
35	545	59.1	1161	10	US-09-891-943-99	Sequence 99, Appl
36	544	59.0	1155	9	US-09-350-259-46	Sequence 46, Appl
37	544	59.0	1155	10	US-09-891-943-46	Sequence 46, Appl
38	544	59.0	1161	9	US-09-350-259-53	Sequence 53, Appl
39	544	59.0	1161	10	US-09-891-943-53	Sequence 53, Appl
40	488	52.9	1163	9	US-09-350-259-4	Sequence 4, Appl
41	488	52.9	1163	10	US-09-891-943-4	Sequence 4, Appl
42	486	52.7	191	10	US-09-805-354-2	Sequence 2, Appl
43	486	52.7	191	11	US-09-758-493-2	Sequence 2, Appl
44	486	52.7	191	14	US-10-144-259-2	Sequence 2, Appl
45	486	52.7	1163	14	US-10-116-275-204	Sequence 204, App

ALIGNMENTS

RESULT 1

US-09-805-354-1
; Sequence 1, Application US/09805354
; Publication No. US20030078375A1
; GENERAL INFORMATION:
; APPLICANT: Arnsout, M. Amin
; APPLICANT: Li, Rui
; APPLICANT: Xiong, Jian-Ping
; TITLE OF INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 00786-536001
; CURRENT APPLICATION NUMBER: US/09/805,354
; PRIOR FILING DATE: 2002-06-04
; PRIOR FILING DATE: 2001-01-11
; PRIOR FILING DATE: 2001-01-11
; PRIOR FILING DATE: 2000-07-31
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-805-354-1

Query Match 97.9%; Score 903; DB 10; Length 191;
Best Local Similarity 99.4%; Pred. No. 6.2e-89;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	CPQEDSDIAFLIDGSGSIIPHDFFRMKKEFVSTVMOLKSKTLFSLMQYSEFRHFTFK	60
Db	1	CPQEDSDIAFLIDGSGSIIPHDFFRMKKEFVSTVMOLKSKTLFSLMQYSEFRHFTFK	60
Qy	61	EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKLVITDGEKFG	120
Db	61	EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKLVITDGEKFG	120

	DPLGYEDV	IPEADREGVI	RVTGVGD	AFRSEKSRQELN	TASKPRDHVFQNFE	176
Qy						
	DPLGYEDV	IPEADREGVI	RVTGVGD	AFRSEKSRQELN	TASKPRDHVFQNFE	176
Db						

RESULT 2

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US-09-758-493-1
; Sequence 1, Application US/09758493
; Publication No. US20040086935A1
; GENERAL INFORMATION:
; APPLICANT: Arnaout, M. Amin
; APPLICANT: Li, Rui
; APPLICANT: Xiong, Jian-Ping
; TITLE OF INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 00786-804001
; CURRENT APPLICATION NUMBER: US/09/758,493
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/221,950
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-758-493-1

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	Query Match	Best Local Similarity	Score 903;	DB 11;	Length 191;
	Matches 175;	Conservative	0;	Mismatches 1;	Indels 0;
					Gaps 0
Qy	1	CQEQSDIAFLIDGSGSII	PHDFRMKEFEVSTVMEQLKSKTILFSLQWYSEERPHFTPK	60	
Db	1	CQEQSDIAFLIDGSGSII	PHDFRMKEFEVSTVMEQLKSKTILFSLQWYSEERPHFTPK	60	
Qy	61	EFQNNPNRSLVKPITQLLGRTHRTATGIRKVVRELFNITNGARKNAFKILWITDGEKFG	120		
Db	61	EFQNNPNRSLVKPITQLLGRTHRTATGIRKVVRELFNITNGARKNAFKILWITDGEKFG	120		
Qy	121	DPLEGYEDVIPADREGVIRYVIGVDGDAFREKSKRQELNNTIASKPPRDHVFQCNFFE	176		
Db	121	DPLEGYEDVIPADREGVIRYVIGVDGDAFREKSKRQELNNTIASKPPRDHVFQCNFFE	176		

RESULT 3

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US-10-144-259-1
; Sequence 1, Application US/10144259
; Publication NO. US20030109691A1
; GENERAL INFORMATION:
; APPLICANT: Arnaout, M. Amin
; APPLICANT: Li, Rui
; APPLICANT: Xiong, Jian-Ping
; TITLE OF INVENTION: VARIANT INTEGRIN POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 00786-548001
; CURRENT APPLICATION NUMBER: US/10/144,259
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: US 09/758,493
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/221,950
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
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; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-259-1

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Qy	1	CPQEDSDIAFLIDGSGSII	PHDPRMKEFVTVMEQLKSKTILFSLMQSYSEFR.IHFTFK	60
Db	1	CPQEDSDIAFLIDGSGSII	PHDPRMKEFVTVMEQLKSKTILFSLMQSYSEFR.IHFTFK	60
Qy	61	BFQNNPNRSLVXPITQLGRTH	TATGIRKVVRELFNITNGARKNAFKILVITDGEKFG	120
Db	61	BFQNNPNRSLVXPITQLGRTH	TATGIRKVVRELFNITNGARKNAFKILVITDGEKFG	120
Qy	121	DP.LGYEDVUIPEADREGVIRVYI	GVGDAPRSKSRQELNTIASKPPRDHVFQCNPE	176
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RESULT 4

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US-09-945-265-4
; Sequence 4, Application US/09945265
; Patent No. US20020123614A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy A.
; APPLICANT: Shimadzu, Motomu
; APPLICANT: Lu, Chafen
; TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A
; TITLE OF INVENTION: DESIRED CONFORMATION AND METHODS FOR PRODUCING SAME
; FILE REFERENCE: CN-002CP
; CURRENT APPLICATION NUMBER: US/09/945,265
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,700
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-945-265-4

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RESULT 5

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US-09-350-259-3
; Sequence 3, Application US/09350259
; Patent No. US20020062008A1
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. US20020062008A1el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/350,259
; CURRENT FILING DATE: 1999-07-08
; EARLIER APPLICATION NUMBER: 09/193,043
; EARLIER FILING DATE: 1998-11-16
; EARLIER APPLICATION NUMBER: 08/173,497
; EARLIER FILING DATE: 1993-12-23
; EARLIER APPLICATION NUMBER: 08/286,889
; EARLIER FILING DATE: 1994-08-05
; EARLIER APPLICATION NUMBER: 08/362,652
; EARLIER FILING DATE: 1994-12-21
; EARLIER APPLICATION NUMBER: 08/943,363

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; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-350-259-3

Query Match          97.9%; Score 903; DB 9; Length 1153;
Best Local Similarity 99.4%; Pred. No. 7.4e-88;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDFRMKFEVSTVMEQLKSKTLFSLMOYSESEFRHFTFK 60
Db 144 CPQEDSDIAFLIDGSGSIIPHDFRMKFEVSTVMEQLKSKTLFSLMOYSESEFRHFTFK 203

QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
Db 204 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263

QY 121 DPLGYEDVIPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVQCNFFE 176
Db 264 DPLGYEDVIPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVQCNFFE 319

RESULT 6
US-09-902-481A-1
; Sequence 1, Application US/09902481A
; Publication No. US2003005440A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy
; APPLICANT: Shimaoka, Motomu
; APPLICANT: Shifman, Julia
; APPLICANT: Mayo, Stephen
; TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
; FILE REFERENCE: A-70586-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/902,481A
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/216,600
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-902-481A-1

Query Match          97.9%; Score 903; DB 10; Length 1153;
Best Local Similarity 99.4%; Pred. No. 7.4e-88;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDFRMKFEVSTVMEQLKSKTLFSLMOYSESEFRHFTFK 60
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Db 204 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263

QY 121 DPLGYEDVIPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVQCNFFE 176
Db 264 DPLGYEDVIPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVQCNFFE 319

RESULT 7
US-09-891-943-3
; Sequence 3, Application US/09891943
; Publication No. US20030077278A1
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. US20030077278A1el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/891,943
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 09/193,043
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/286,889
; PRIOR FILING DATE: 1994-08-05
; PRIOR APPLICATION NUMBER: 08/362,652
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/943,363
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-891-943-3

Query Match          97.9%; Score 903; DB 10; Length 1153;
Best Local Similarity 99.4%; Pred. No. 7.4e-88;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDFRMKFEVSTVMEQLKSKTLFSLMOYSESEFRHFTFK 60
Db 144 CPQEDSDIAFLIDGSGSIIPHDFRMKFEVSTVMEQLKSKTLFSLMOYSESEFRHFTFK 203

QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
Db 204 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263

QY 121 DPLGYEDVIPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVQCNFFE 176
Db 264 DPLGYEDVIPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVQCNFFE 319

RESULT 8
US-10-144-259-30
; Sequence 30, Application US/10144259
; Publication No. US20030109691A1
; GENERAL INFORMATION:
; APPLICANT: Arnaout, M. Amin
; APPLICANT: Li, Rui
; APPLICANT: Xiong, Jian-Ping
; TITLE OF INVENTION: VARIANT INTEGRIN POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 00786-548001
; CURRENT APPLICATION NUMBER: US/10/144,259
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: US 09/758,493
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/221,950
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-259-30

Query Match          97.9%; Score 903; DB 14; Length 1153;
Best Local Similarity 99.4%; Pred. No. 7.4e-88;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDFRMKFEVSTVMEQLKSKTLFSLMOYSESEFRHFTFK 60
Db 144 CPQEDSDIAFLIDGSGSIIPHDFRMKFEVSTVMEQLKSKTLFSLMOYSESEFRHFTFK 203
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61	EQNNPNPSLWKPI	TOLLGRTH	TATGIRKVVREL	FNI	TNGARKNAP	KIL	LWITDGEK	120
Qy								
204	EQNNPNPSLWKPI	TOLLGRTH	TATGIRKVVREL	FNI	TNGARKNAP	KIL	LWITDGEK	263
Db								
121	DPGLVEDVI	PEADREGVI	YVIGVDAP	FRSEK	QELNT	IASPP	PRDHV	176
Qy								
264	DPGLVEDVI	PEADREGVI	YVIGVDAP	FRSEK	QELNT	IASPP	PRDHV	319
Db								

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RESULT 9
US-10-207-655-176
; Sequence 176, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069 401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 176
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-176

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Query Match	97.9%	Score 903;	DB 14;	Length 1153;
Best Local Similarity	99.4%;	Pred. No. 7.4e-88;		
Matches 175; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

Qy	1	CQ	Q	S	D	I	A	F	L	I	D	G	S	I	I	P	H	D	F	R	M	K	E	F	V	T	N	M	E	Q	L	K	S	K	T	F	S	L	M	Q	S	E	E	R	I	H	T	F	K	60								
Db	144	CQ	Q	S	D	I	A	F	L	I	D	G	S	I	I	P	H	D	F	R	M	K	E	F	V	T	N	M	E	Q	L	K	S	K	T	F	S	L	M	Q	S	E	E	R	I	H	T	F	K	203								
Qy	61	E	F	Q	N	N	P	R	S	L	V	K	P	T	O	L	L	G	R	T	H	T	A	T	G	I	R	K	V	V	R	E	L	F	N	I	T	N	G	A	R	K	N	A	F	K	I	L	V	I	T	D	G	E	K	F	G	120
Db	204	E	F	Q	N	N	P	R	S	L	V	K	P	T	O	L	L	G	R	T	H	T	A	T	G	I	R	K	V	V	R	E	L	F	N	I	T	N	G	A	R	K	N	A	F	K	I	L	V	I	T	D	G	E	K	F	G	263
Qy	121	D	P	L	G	H	E	D	V	I	P	E	A	D	R	G	V	I	Y	I	G	V	D	A	P	R	S	K	S	Q	E	L	N	T	I	A	S	K	P	R	H	D	V	F	Q	C	N	N	F	E	176							
Db	264	D	P	L	G	H	E	D	V	I	P	E	A	D	R	G	V	I	Y	I	G	V	D	A	P	R	S	K	S	Q	E	L	N	T	I	A	S	K	P	R	H	D	V	F	Q	C	N	N	F	E	319							

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RESULT 10
US-09-902-481A-6
; Sequence 6, Application US/09902481A
; Publication No. US20030054440A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy
; APPLICANT: Shimooka, Motomu
; APPLICANT: Shifman, Julia
; APPLICANT: Mayo, Stephen
; TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
; FILE REFERENCE: A-70586-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/902,481A
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/216,600
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 1137
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-902-481A-6

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Query Match	97.0%	Score 894;	DB 10;	Length 1137;
Best Local Similarity	97.2%	Pred. No. 6.7e-87;		
Matches 171; Conservative	3;	Mismatches 2;	Indels 0	

Qy	1	CPQEDSDIAFLIDGSGSII	PHDFPRMKFVSTVMQLKSKSTLPSLMQYSEFR	IHTFTK	60
Db	128	CPQEDSDIAFLIDGSGSII	PHDFPRMKFVSTVMQLKSKSTLPSLMQYSEFR	IHTFTK	187
Qy	61	EFQNNPNPSRLVKPIT	OLLGRTHTATGIRKVVRELFNITGARKNAFKIL	VITDGEKFG	120
Db	188	EFQNNPNPSRLVKPIT	OLLGRTHTATGVRKVIPELLNITGARKNAFKIL	VITDGEKFG	247
Qy	121	DPGLGYEDVIEADREGVIRYVI	GVGDAPRSEKSRQELNTIIASKPPRDHV	FQCNNE	176
Db	248	DPGLGYEDVIEADREGVIRYVI	GVGDAPRSEKSRQELNTIIASKPPRDHV	FQCNNE	303

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RESULT 11
US-09-902-481A-5
; Sequence 5, Application US/09902481A
; Publication No. US20030054440A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy
; APPLICANT: Shimaoka, Motomu
; APPLICANT: Shifman, Julia
; APPLICANT: Mayo, Stephen
; TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
; FILE REFERENCE: A-70586-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/902,481A
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/216,600
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1137
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-902-481A-5

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Query Match	96.4%	Score 889;	DB 10;	Length 1137;
Best Local Similarity	95.5%;	Pred. No. 2.3e-86;		
Matches 168; Conservative	6;	Mismatches 2;	Indels 0;	Gaps 0;

Qy	1	CPQEDSDIAFLIDGSGSIIIPHDFFRMKEFVSTMVQQLKSKTILFSLMQYSEFRHHTFK	60
Db	128	CPQEDSDIAFLVDGSGSIIIPHDFFRAKEFISTVMQQLKSKTILFSLMQYSEFRHHTFK	187
Qy	61	EFQNNPNPRSLVPIITOLLGRTHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG	120
Db	188	EFQNNPNPRSLIKPITQLGRTHTATGIRKVVRELFNITNGARKNAFKILITDGEKFG	247
Qy	121	DPLGYEDVIEADREGVIRYVIGVDAFRSEKSRQELNTIASKPPRDHVQCNNEF	176
Db	248	DPLGYEDVIEADREGVIRYVIGVDAFRSEKSRQELNTVASKPPRDHVQINNPF	303

RESULT 12
US-09-302-481A-4
; Sequence 4, Application US/09902481A
; Publication No. US20030054440A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy
; APPLICANT: Shimazaki, Motomu
; APPLICANT: Shifman, Julia
; APPLICANT: Mayo, Stephen
; TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
; FILE REFERENCE: A-70586-1/RPT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/902,481A
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/216,600
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 4
; LENGTH: 1137
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-902-481A-4

Query Match          95.3%; Score 879; DB 10; Length 1137;
Best Local Similarity 94.9%; Pred. No. 2.8e-85;
Matches 167; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTK 60
DB 128 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTK 187
QY 61 EFQNNPNSLVKPIITQLLGRTHGTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 188 EFQNNPNSLVKPIITQLLGRTHGTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 247
QY 121 DPLGYVEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVQCNFFE 176
DB 248 DPLGYVEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVQCNFFE 303

RESULT 13
US-10-346-863-17
; Sequence 17, Application US/10346863
; Publication No. US20040038325A1
; GENERAL INFORMATION:
; APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
; APPLICANT: FAGAN, RICHARD JOSEPH
; APPLICANT: GUTTERIDGE, ALEX
; TITLE OF INVENTION: ADHESION MOLECULES
; FILE REFERENCE: 674575-2001
; CURRENT APPLICATION NUMBER: US/10/346,863
; CURRENT FILING DATE: 2003-01-17
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: GB 0018126.3
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: GB 0025447.4
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-346-863-17

Query Match          95.1%; Score 877; DB 15; Length 184;
Best Local Similarity 94.4%; Pred. No. 3.8e-86;
Matches 171; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTK 64
DB 1 DSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTK 60
QY 65 NPNPSLVKPIITQLLGRTHGTATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLG 124
DB 61 NPNPSLVKPIITQLLGRTHGTATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLG 120

RESULT 14
US-10-346-863-37
; Sequence 37, Application US/10346863
; Publication No. US20040038325A1
; GENERAL INFORMATION:
; APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
; APPLICANT: FAGAN, RICHARD JOSEPH
; APPLICANT: GUTTERIDGE, ALEX
; TITLE OF INVENTION: ADHESION MOLECULES
; FILE REFERENCE: 674575-2001
; CURRENT APPLICATION NUMBER: US/10/346,863
; CURRENT FILING DATE: 2003-01-17
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: GB 0018126.3
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: GB 0025447.4
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-346-863-37

Query Match          95.1%; Score 877; DB 16; Length 187;
Best Local Similarity 99.4%; Pred. No. 3.9e-86;
Matches 171; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTK 64
DB 1 DSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTK 60
QY 65 NPNPSLVKPIITQLLGRTHGTATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLG 124
DB 61 NPNPSLVKPIITQLLGRTHGTATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLG 120
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; APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
; APPLICANT: FAGAN, RICHARD JOSEPH
; APPLICANT: GUTTERIDGE, ALEX
; TITLE OF INVENTION: ADHESION MOLECULES
; FILE REFERENCE: 674575-2001
; CURRENT APPLICATION NUMBER: US/10/346,863
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: PCT/GB01/03318
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: GB 0018126.3
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: GB 0025447.4
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-346-863-37

Query Match          95.1%; Score 877; DB 15; Length 187;
Best Local Similarity 99.4%; Pred. No. 3.9e-86;
Matches 171; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTK 64
DB 1 DSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTK 60
QY 65 NPNPSLVKPIITQLLGRTHGTATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLG 124
DB 61 NPNPSLVKPIITQLLGRTHGTATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLG 120

RESULT 15
US-10-615-515-9
; Sequence 9, Application US/10615515
; Publication No. US20040132974A1
; GENERAL INFORMATION:
; APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
; APPLICANT: FAGAN, RICHARD JOSEPH
; APPLICANT: GUTTERIDGE, ALEX
; TITLE OF INVENTION: ADHESION MOLECULES
; FILE REFERENCE: 674575-2004
; CURRENT APPLICATION NUMBER: US/10/615,515
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: PCT/GB02/00107
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: GB 0100750.9
; PRIOR FILING DATE: 2001-01-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 9
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-615-515-9

Query Match          95.1%; Score 877; DB 16; Length 187;
Best Local Similarity 99.4%; Pred. No. 3.9e-86;
Matches 171; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTK 64
DB 1 DSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTK 60
QY 65 NPNPSLVKPIITQLLGRTHGTATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLG 124
DB 61 NPNPSLVKPIITQLLGRTHGTATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLG 120
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Qy 125 YEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNPE 176
Db 121 YEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQNNPE 172

Search completed: January 13, 2005, 15:39:45
Job time : 30.2475 secs

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OM protein - protein search, using sw model

Run on: January 13, 2005, 15:07:42 ; Search time 8.50625 Seconds
(without alignments)
1379.959 Million cell updates/sec

Title: RWHULB-C_COPY_144_320

Perfect score: 922

Sequence: 1 CPQEDSDIAFLIDSGSIIP.....NTIASKPRDRHVQCNNEC 177

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Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

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- 2: /cgn2_6/ptodata/1/1aa/5B-COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/6A-COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6B-COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS-COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	903	97.9	187	2	US-08-177-109A-61
2	903	97.9	187	2	US-08-687-706-61
3	903	97.9	1152	2	US-08-476-062A-43
4	903	97.9	1152	5	PCT-US96-01314-43
5	903	97.9	1152	6	5424399-2
6	903	97.9	1153	1	US-08-173-497-3
7	903	97.9	1153	1	US-08-286-889-3
8	903	97.9	1153	1	US-08-485-618-3
9	903	97.9	1153	1	US-08-362-652-3
10	903	97.9	1153	2	US-08-605-672-3
11	903	97.9	1153	2	US-08-482-293A-3
12	903	97.9	1153	2	US-08-943-363-3
13	903	97.9	1153	3	US-09-193-043-3
14	903	97.9	1153	4	US-09-688-307A-3
15	903	97.9	1153	4	US-09-350-259-3
16	871	94.5	216	4	US-09-795-872-5
17	871	94.5	435	5	PCT-US95-04439-1
18	559	60.6	413	1	US-08-485-618-101
19	559	60.6	413	2	US-08-605-672-101
20	559	60.6	413	2	US-08-482-293A-101
21	559	60.6	413	2	US-08-943-363-101
22	559	60.6	413	3	US-09-193-043-101
23	559	60.6	413	4	US-09-688-307A-101
24	559	60.6	413	4	US-09-350-259-101
25	550	59.7	1151	1	US-08-286-889-37
26	550	59.7	1151	1	US-08-485-618-37
27	550	59.7	1151	1	US-08-362-652-37

28	550	59.7	1151	2	US-08-605-672-37	Sequence 37, Appl
29	550	59.7	1151	2	US-08-482-293A-37	Sequence 37, Appl
30	550	59.7	1151	2	US-08-943-363-37	Sequence 37, Appl
31	550	59.7	1151	3	US-09-193-043-37	Sequence 37, Appl
32	550	59.7	1151	4	US-09-688-307A-37	Sequence 37, Appl
33	550	59.7	1151	4	US-09-350-259-37	Sequence 37, Appl
34	550	59.7	1161	1	US-08-485-618-55	Sequence 55, Appl
35	550	59.7	1161	1	US-08-362-652-55	Sequence 55, Appl
36	550	59.7	1161	2	US-08-605-672-55	Sequence 55, Appl
37	550	59.7	1161	2	US-08-482-293A-55	Sequence 55, Appl
38	550	59.7	1161	2	US-08-943-363-55	Sequence 55, Appl
39	550	59.7	1161	3	US-09-193-043-55	Sequence 55, Appl
40	550	59.7	1161	4	US-09-688-307A-55	Sequence 55, Appl
41	550	59.7	1161	4	US-09-350-259-55	Sequence 55, Appl
42	545	59.1	1161	1	US-08-173-497-2	Sequence 2, Appl
43	545	59.1	1161	1	US-08-286-889-2	Sequence 2, Appl
44	545	59.1	1161	1	US-08-485-618-2	Sequence 2, Appl
45	545	59.1	1161	1	US-08-485-618-99	Sequence 99, Appl

ALIGNMENTS

RESULT 1
US-08-177-109A-61
; Sequence 61, Application US/08177109A
; Patent No. 5869615
; GENERAL INFORMATION:
; APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby
; TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/177,109A
; FILING DATE: 03-JAN-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: WU 107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-177-109A-61

Query Match 97.9%; Score 903; DB 2; Length 187;
Best Local Similarity 99.4%; Pred. No. 8.9e-93;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CPQEDSDIAFLIDSGSIIPPHDFRMKEFVSVTMVQKSKTFLFSLMQYSEEFRIHFTFK 60
DB 1 CPQEDSDIAFLIDSGSIIPPHDFRMKEFVSVTMVQKSKTFLFSLMQYSEEFRIHFTFK 60
QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120

Db 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 120
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFSEKSRQELNTIASKPPRDHVFQCNFFE 176
Db 121 DPLGYEDVIPADREGVIRYVIGVDAPFSEKSRQELNTIASKPPRDHVFQCNFFE 176

RESULT 2

US-08-687-706-61
; Sequence 61, Application US/08687706
; Patent No. 5928892
; GENERAL INFORMATION:
; APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby
; TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,706
; FILING DATE: 26-JUL-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/177,109
; FILING DATE: 03-JAN-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: WU 107 DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-687-706-61

Query Match 97.9%; Score 903; DB 2; Length 187;
Best Local Similarity 99.4%; Pred. No. 8.9e-93;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60
Db 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60
QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 120
Db 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 120
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFSEKSRQELNTIASKPPRDHVFQCNFFE 176
Db 121 DPLGYEDVIPADREGVIRYVIGVDAPFSEKSRQELNTIASKPPRDHVFQCNFFE 176

RESULT 3

US-08-476-062A-43
; Sequence 43, Application US/08476062A

; Patent No. 5877275
; GENERAL INFORMATION:
; APPLICANT: Arnaout, M. Amin
; TITLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,062A
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/216,081
; FILING DATE: 21-MAR-1994
; APPLICATION NUMBER: 07/637,830
; FILING DATE: 04-JAN-1991
; APPLICATION NUMBER: 07/539,842
; FILING DATE: 18-JUN-1990
; APPLICATION NUMBER: 07/212,573
; FILING DATE: 28-JUN-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00786/068003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1152 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-476-062A-43

Query Match 97.9%; Score 903; DB 2; Length 1152;
Best Local Similarity 99.4%; Pred. No. 1e-91;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60
Db 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 120
Db 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFSEKSRQELNTIASKPPRDHVFQCNFFE 176
Db 264 DPLGYEDVIPADREGVIRYVIGVDAPFSEKSRQELNTIASKPPRDHVFQCNFFE 319
RESULT 4
PCT-US96-01314-43
; Sequence 43, Application PC/TUS9601314
; GENERAL INFORMATION:
; APPLICANT: M. Amin Arnaout
; TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:

; ADDRESSEZ: Fish & Richardson P.C.
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; COMPUTER: IBM PS/2 Model 502 or 55SX
 ; OPERATING SYSTEM: MS-DOS (Version 5.0)
 ; SOFTWARE: WordPerfect (Version 5.1)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US96/01314
 ; FILING DATE: 30-JAN-96
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/380,167
 ; FILING DATE: 30-JAN-95
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: John W. Freeman
 ; REGISTRATION NUMBER: 29,066
 ; REFERENCE/DOCKET NUMBER: 00786/267001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 542-5070
 ; TELEFAX: (617) 542-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 43:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1152
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear.
 ; PCT-US96-01314-43

Query Match 97.9%; Score 903; DB 5; Length 1152;
 Best Local Similarity 99.4%; Pred. No. 1e-91;
 Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CPQEDSDIAFLIDGSGSIIPHDFFRMKGFVSTVMEQLKSKTFLSLMQYSEEFRIHFTPK 60
 DB 144 CPQEDSDIAFLIDGSGSIIPHDFFRMKGFVSTVMEQLKSKTFLSLMQYSEEFRIHFTPK 203
 QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
 DB 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
 QY 121 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQCNFFE 176
 DB 264 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQCNFFE 319

RESULT 5
 5424399-2
 ; Patent No. 5424399
 ; APPLICANT: ARNAOUT, M. AMIN
 ; TITLE OF INVENTION: HUMAN CR3a/b HETERODIMERS
 ; NUMBER OF SEQUENCES: 12
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/78,871
 ; FILING DATE: 16-JUN-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 539,842
 ; FILING DATE: 18-JUN-1990
 ; APPLICATION NUMBER: 212,573
 ; FILING DATE: 28-JUN-1988
 ; SEQ ID NO: 2:
 ; LENGTH: 1152
 ; 5424399-2

Query Match 97.9%; Score 903; DB 6; Length 1152;
 Best Local Similarity 99.4%; Pred. No. 1e-91;
 Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDFFRMKGFVSTVMEQLKSKTFLSLMQYSEEFRIHFTPK 60

DB 144 CPQEDSDIAFLIDGSGSIIPHDFFRMKGFVSTVMEQLKSKTFLSLMQYSEEFRIHFTPK 203
 QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
 DB 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
 QY 121 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQCNFFE 176
 DB 264 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQCNFFE 319

RESULT 6

US-08-173-497-3
 ; Sequence 3, Application US/08173497
 ; Patent No. 5437958
 ; GENERAL INFORMATION:
 ; APPLICANT: Gallatin, W. Michael
 ; APPLICANT: Van Der Vieren, Monica
 ; TITLE OF INVENTION: No. 5437958el Human 2 Integrin Alpha
 ; TITLE OF INVENTION: Subunit
 ; NUMBER OF SEQUENCES: 29
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 233 S. Wacker Drive, 6300 Sears Tower
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/173,497
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 5437958and, Greta E.
 ; REGISTRATION NUMBER: 35,302
 ; REFERENCE/DOCKET NUMBER: 27866/31363
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-474-6300
 ; TELEFAX: 312-474-0448
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1153 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-173-497-3

Query Match 97.9%; Score 903; DB 1; Length 1153;
 Best Local Similarity 99.4%; Pred. No. 1e-91;
 Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDFFRMKGFVSTVMEQLKSKTFLSLMQYSEEFRIHFTPK 60
 DB 144 CPQEDSDIAFLIDGSGSIIPHDFFRMKGFVSTVMEQLKSKTFLSLMQYSEEFRIHFTPK 203
 QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
 DB 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
 QY 121 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQCNFFE 176
 DB 264 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQCNFFE 319

RESULT 7

US-08-286-889-3
; Sequence 3, Application US/08286889
; Patent No. 5470953
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,889
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: P38,659
; REFERENCE/DOCKET NUMBER: 27866/32168
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1153 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-286-889-3
Query Match 97.9%; Score 903; DB 1; Length 1153;
Best Local Similarity 99.4%; Pred. No. 1e-91;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CPQSDSIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMYSSEFRIHFTFK 60
DB 144 CPQSDSIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMYSSEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQNNFE 176
DB 264 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQNNFE 319
RESULT 8
US-08-485-618-3
; Sequence 3, Application US/08485618
; Patent No. 5728533
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower

; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,618
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32797
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1153 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-485-618-3
Query Match 97.9%; Score 903; DB 1; Length 1153;
Best Local Similarity 99.4%; Pred. No. 1e-91;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CPQSDSIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMYSSEFRIHFTFK 60
DB 144 CPQSDSIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMYSSEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQNNFE 176
DB 264 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQNNFE 319
RESULT 9
US-08-362-652-3
; Sequence 3, Application US/08362652
; Patent No. 5766850
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
FILING DATE: 5-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-362-652-3

Query Match 97.9%; Score 903; DB 1; Length 1153;
Best Local Similarity 99.4%; Pred. No. 1e-91;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CPQSDSIAFLIDSGSIIPHDFFRMKFEVSTVMEQLKSKTLPFLSMQYSEEFRIHFTFK 60
DB 144 CPQSDSIAFLIDSGSIIPHDFFRMKFEVSTVMEQLKSKTLPFLSMQYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNTNGARKNAFKILVVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNTNGARKNAFKILVVITDGEKFG 263
QY 121 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQCNFE 176
DB 264 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQCNFE 319

RESULT 10
US-08-605-672-3
Sequence 3, Application US/08605672
Patent No. 5817515
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE: 530
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-605-672-3

Query Match 97.9%; Score 903; DB 2; Length 1153;
Best Local Similarity 99.4%; Pred. No. 1e-91;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CPQSDSIAFLIDSGSIIPHDFFRMKFEVSTVMEQLKSKTLPFLSMQYSEEFRIHFTFK 60
DB 144 CPQSDSIAFLIDSGSIIPHDFFRMKFEVSTVMEQLKSKTLPFLSMQYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNTNGARKNAFKILVVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNTNGARKNAFKILVVITDGEKFG 263
QY 121 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQCNFE 176
DB 264 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQCNFE 319

RESULT 11
US-08-482-293A-3
Sequence 3, Application US/08482293A
Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
FILING DATE: 530
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889

```
/ FILING DATE: 5-AUG-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/362,652
/ FILING DATE: 21-DEC-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27866/32684
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1153 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-482-293A-3

Query Match          97.9%; Score 903; DB 2; Length 1153;
Best Local Similarity 99.4%; Pred. No. 1e-91;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDFFRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60
Db 144 CPQEDSDIAFLIDGSGSIIPHDFFRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
Db 204 EFQNNPNRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQNNPE 176
Db 264 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQNNPE 319

RESULT 12
US-08-943-363-3
/ Sequence 3, Application US/08943363
/ Patent No. 5837478
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, W. Michael
/ APPLICANT: Van der Vieren, Monica
/ TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
/ NUMBER OF SEQUENCES: 114
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 233 South Wacker Drive, 6300 Sear Tower
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States
/ ZIP: 60606-6402
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/943,363
/ FILING DATE:
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/286,889
/ FILING DATE: 5-AUG-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/362,652
/ FILING DATE: 21-DEC-1994
/ ATTORNEY/AGENT INFORMATION:
```

```
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27866/32684
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1153 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-943-363-3

Query Match          97.9%; Score 903; DB 2; Length 1153;
Best Local Similarity 99.4%; Pred. No. 1e-91;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDFFRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60
Db 144 CPQEDSDIAFLIDGSGSIIPHDFFRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
Db 204 EFQNNPNRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQNNPE 176
Db 264 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQNNPE 319

RESULT 13
US-08-193-043-3
/ Sequence 3, Application US/09193043
/ Patent No. 6251395
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, Michael W.
/ APPLICANT: Van der Vieren, Monica
/ TITLE OF INVENTION: No. 6251395el Human 2
/ FILE REFERENCE: 27866/35004
/ CURRENT APPLICATION NUMBER: US/09/193,043
/ CURRENT FILING DATE: 1998-11-16
/ EARLIER APPLICATION NUMBER: 08/173,497
/ EARLIER FILING DATE: 1993-12-23
/ EARLIER APPLICATION NUMBER: 08/286,889
/ EARLIER FILING DATE: 1994-08-05
/ EARLIER APPLICATION NUMBER: 08/362,652
/ EARLIER FILING DATE: 1994-12-21
/ EARLIER APPLICATION NUMBER: 08/943,363
/ EARLIER FILING DATE: 1997-10-03
/ NUMBER OF SEQ ID NOS: 114
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 3
/ LENGTH: 1153
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-193-043-3

Query Match          97.9%; Score 903; DB 3; Length 1153;
Best Local Similarity 99.4%; Pred. No. 1e-91;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDFFRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60
Db 144 CPQEDSDIAFLIDGSGSIIPHDFFRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
Db 204 EFQNNPNRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQNNPE 176
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Db 264 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFE 319
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RESULT 14

US-09-688-307A-3
; Sequence 3, Application US/09688307A
; Patent No. 6432404
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 6432404el Human Beta-2
; FILE REFERENCE: 27866/36646
; CURRENT APPLICATION NUMBER: US/09/688,307A
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 09/193,043
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/605,672
; PRIOR FILING DATE: 1996-02-22
; PRIOR APPLICATION NUMBER: 08/173,497
; PRIOR FILING DATE: 1993-12-23
; PRIOR APPLICATION NUMBER: 08/286,889
; PRIOR FILING DATE: 1994-08-05
; PRIOR APPLICATION NUMBER: 08/362,652
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/943,363
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-688-307A-3

Query Match 97.9%; Score 903; DB 4; Length 1153;
Best Local Similarity 99.4%; Pred. No. 1e-91;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLGRTHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
Db 204 EFQNNPNRSLVKPITQLGRTHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFE 176
Db 264 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFE 319

RESULT 15

US-09-350-259-3
; Sequence 3, Application US/09350259
; Patent No. 6620915
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 6620915el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/350,259
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 09/193,043
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/173,497
; PRIOR FILING DATE: 1993-12-23
; PRIOR APPLICATION NUMBER: 08/286,889
; PRIOR FILING DATE: 1994-08-05
; PRIOR APPLICATION NUMBER: 08/362,652
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/943,363
; PRIOR FILING DATE: 1997-10-03

; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-350-259-3
Query Match 97.9%; Score 903; DB 4; Length 1153;
Best Local Similarity 99.4%; Pred. No. 1e-91;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTFK 203
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Db 204 EFQNNPNRSLVKPITQLGRTHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFE 176
Db 264 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFE 319

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